

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 11, 2005, 17:39:11 ; Search time 89.0148 Seconds  
(without alignments)  
373.662 Million cell updates/sec

Title: US-10-054-873-4  
Perfect score: 463  
Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	8 Query		DB	ID	Description
		Match	Length			
1	463	100.0	86	1	AAP40829	Aap40829 Sequence
2	463	100.0	86	2	AAR84061	Aar84061 Human ins
3	463	100.0	86	2	AAY42858	Aay42858 Human ins
4	463	100.0	86	3	AAB12770	Aab12770 Human pro
5	463	100.0	86	5	AAM48218	Aam48218 Human pro
6	463	100.0	86	7	ADC64463	Adc64463 Amino aci
7	463	100.0	86	7	ADF16632	Adf16632 Human alb
8	463	100.0	86	7	ADH21860	Adh21860 Human lon
9	463	100.0	86	8	ADT93277	Adt93277 Human nat

10	463	100.0	87	1	AAP20036	Aap20036	Human pro
11	463	100.0	87	1	AAP40217	Aap40217	Sequence
12	463	100.0	87	1	AAP50127	Aap50127	Sequence
13	463	100.0	87	1	AAP50060	Aap50060	Synthetic
14	463	100.0	87	1	AAP61090	Aap61090	Sequence
15	463	100.0	87	2	AAR32367	Aar32367	Proinsuli
16	463	100.0	88	2	AAR07682	Aar07682	Modified
17	463	100.0	88	2	AAR33855	Aar33855	hpI. 3/20
18	463	100.0	92	2	AAR20467	Aar20467	Yeast alp
19	463	100.0	92	8	ADL24442	Adl24442	Modified
20	463	100.0	93	1	AAP90102	Aap90102	Synthetic
21	463	100.0	96	2	AA08004	Aay08004	Human pro
22	463	100.0	96	2	AA017830	Aao17830	Human pro
23	463	100.0	96	8	ADL24437	Adl24437	Modified
24	463	100.0	97	2	AAR68898	Aar68898	Human pro
25	463	100.0	97	3	AAB12773	Aab12773	Human pro
26	463	100.0	110	1	AAP10042	Aap10042	Sequence
27	463	100.0	110	1	AAP10053	Aap10053	Sequence
28	463	100.0	110	1	AAP40309	Aap40309	Sequence
29	463	100.0	110	2	AA06608	Aay06608	Human pre
30	463	100.0	110	2	ADF77582	Adf77582	Human ins
31	463	100.0	110	3	AA044367	Aay44367	Human pro
32	463	100.0	110	3	AA070366	Aay70366	Human Ins
33	463	100.0	110	3	AAB26765	Aab26765	Human pre
34	463	100.0	110	3	AAB06144	Aab06144	Human ins
35	463	100.0	110	4	AAE10337	Aae10337	Human pre
36	463	100.0	110	4	AAB35424	Aab35424	Secretory
37	463	100.0	110	4	AAG65677	Aag65677	Human pro
38	463	100.0	110	5	ABG60634	Abg60634	Human ins
39	463	100.0	110	5	ABG31590	Abg31590	Human pre
40	463	100.0	110	6	ABR55862	Abr55862	Humanised
41	463	100.0	110	6	ADA09218	Ada09218	Human Pre
42	463	100.0	110	7	ADC51569	Adc51569	Human pro
43	463	100.0	110	7	ADE56710	Ade56710	Human Pro
44	463	100.0	110	7	ADD46938	Add46938	Human Pro
45	463	100.0	110	7	ADE57650	Ade57650	Human Pro

# ALIGNMENTS

## RESULT 1

AAP40829

ID AAP40829 standard; protein; 86 AA.

XX

AC AAP40829;

XX

DT 09-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 03-AUG-1992 (first entry)

XX

DE Sequence of human insulin precursor.

XX

KW Insulin precursor; connecting peptide; diabetes; hormone.

XX

OS Homo sapiens.

OS Unidentified.

XX  
 FH Key Location/Qualifiers  
 FT Region 1. .30  
 FT /label= chain B  
 FT Modified-site 1  
 FT /label= F-NH2-R  
 FT /note= "H or a chemically or enzymatically cleavable AA  
 FT residue or peptide residue"  
 FT Disulfide-bond 7. .72  
 FT Disulfide-bond 19. .85  
 FT Peptide 31. .65  
 FT /label= connecting peptide  
 FT Region 66. .86  
 FT /label= chain A  
 FT Disulfide-bond 71. .76  
 FT Modified-site 86  
 FT /label= N-OH  
 XX  
 PN US4430266-A.  
 XX  
 PD 07-FEB-1984.  
 XX  
 PF 16-FEB-1982; 82US-00349397.  
 XX  
 PR 27-MAR-1980; 80US-00134389.  
 PR 28-NOV-1980; 80US-00210696.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Frank BH;  
 XX  
 DR WPI; 1984-049032/08.  
 XX  
 PT Insulin precursor prodn. from linear S-sulphonate and mercaptan - in  
 PT single step without separate oxidn.  
 XX  
 PS Claim 17; Col 4; 8pp; English.  
 XX  
 CC The inventors claim a method for the prepn. of an insulin precursor in  
 CC which the A-chain and B-chain are joined through a connecting peptide.  
 CC The connecting peptide joins the A-chain at the amino group of A-1 to the  
 CC B-chain at the carboxyl group of B-30. The method is pref. for the prepn.  
 CC of human insulin precursor (see AAP40829). The SQs of the connecting  
 CC peptides of a number of species are given (see AAP40828, AAP40830-39).  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key  
 XX  
 SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 1; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

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Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
```

## RESULT 2

ID AAR84061 standard; protein; 86 AA.

AC    AAR84061;

DT 22-AUG-1996 (first entry)

DE Human insulin.

KW Insulin; transformation; gene expression; fungi; fungal cell; hormone;

KW A-chain; C-chain; glycosylation.

OS Homo sapiens.

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	1. .261
----	-----	---------

```
FT          /*tag=  a
```

FT /product= "Insulin."

PN EP704527-A2.

PD 03-APR-1996.

PF 03-AUG-1995; 95EP-00112210.

PR 05-AUG-1994; 94HR-00000432.

PA (PLIV ) PLIVA PHARM & CHEM FAB.

PI Mestric S, Punt PJ, Valinger R, Van Den Hondel CAMJJ;

DR WPI; 1996-129917/18.

DR N-PSDB; AAT17830, AAT17831.

PT DNA encoding human insulin precursors - which comprise B- and A-chains

PT linked via amino acid chain contg. 1 or more glycosylation sites, for

PT prepn. of insulin in fungal cells.

PS Disclosure; Fig 1; 32pp; English.

CC DNA sequences encoding insulin precursors of formula B-Pg-A, where B and  
CC A represent B- and A-chains of insulin respectively, and Pg represents a  
CC modified C-peptide or any number of amino acids comprising at least one  
CC glycosylation consensus site, can be inserted into expression vectors  
CC which in turn can be used to transform fungal host cells. The fungal  
CC cells are then cultured and the insulin expressed in such cells can be  
CC harvested

SQ Sequence 86 AA;





CC of recombinant human insulin via an hGH-proinsulin chimeric protein can  
 CC provide human insulin with correctly linked cysteine bridges with fewer  
 CC necessary procedural steps, and hence resulting in a higher yield of  
 CC human insulin. The IMC sequences not only protect insulin sequences from  
 CC intracellular degradation by a microorganism host, but also promote the  
 CC folding of the fused insulin precursor, facilitate the solubility of the  
 CC fusion protein and decrease the intermolecular interactions among the  
 CC fusion proteins, thus allowing folding of the fused insulin precursor at  
 CC commercially useful high concentrations. The procedural steps of cyanogen  
 CC bromide cleavage, oxidative sulphitolysis and related purification steps  
 CC can thus be eliminated, along with the use of high concentrations of  
 CC mercaptan or the use of hydrophobic absorbent resins

XX

SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 2; Length 86;

Best Local Similarity 100.0%; Pred. No. 1.5e-43;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 |||

Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 |||

Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

#### RESULT 4

AAB12770

ID AAB12770 standard; protein; 86 AA.

XX

AC AAB12770;

XX

DT 22-NOV-2000 (first entry)

XX

DE Human proinsulin protein sequence SEQ ID NO:2.

XX

KW Human; insulin-like growth factor 1; IGF-1; proinsulin; insulin; mutant;  
 KW variant; insulin-like growth factor binding protein; IGFBP-1; IGFBP-3;  
 KW antidiabetic; neuroprotective; anorectic; tranquilliser; vulnerary;  
 KW anorectic; cardiatic; nephrotropic; dermatological; antiHIV; antiviral;  
 KW hyperglycaemia; obesity; lung disease; glomerulonephritis;  
 KW interstitial nephritis; Turner's syndrome; Laron's syndrome;  
 KW short stature; increased fat mass-to-lean ratio; immunological disorder;  
 KW peripheral neuropathy; multiple sclerosis; muscular dystrophy;  
 KW catabolic state; trauma; wounding; infection; HIV; skin disorder;  
 KW human immunodeficiency virus; diabetes; heart dysfunction;  
 KW kidney disorder; whole body growth disorder.

XX

OS Homo sapiens.

XX

PN WO200040612-A1.

XX

PD 13-JUL-2000.

XX

PF 05-JAN-2000; 2000WO-US000151.



AC AAM48218;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE Human proinsulin.  
 XX  
 KW Antirheumatic; antiarthritic; osteopathic; cartilage disorder;  
 KW insulin-like growth factor; IGF; binding protein; IGFBP;  
 KW rheumatoid arthritis; osteoarthritis; proinsulin; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200187323-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 16-MAY-2001; 2001WO-US015904.  
 XX  
 PR 16-MAY-2000; 2000US-0204490P.  
 PR 15-NOV-2000; 2000US-0248985P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Dubaquié Y, Filvaroff EH, Lowman HB;  
 XX  
 DR WPI; 2002-082942/11.  
 XX  
 PT Treating cartilage disorders including cartilage damage by injury or  
 PT degenerative cartilagenous disorders, by contacting cartilage with  
 PT insulin-like growth factor analog with altered affinity for IGF-binding  
 PT proteins.  
 XX  
 PS Disclosure; Fig 16; 136pp; English.  
 XX  
 CC The present invention relates to a method for treating cartilage  
 CC disorders. The method comprises contacting cartilage with an active agent  
 CC such as insulin-like growth factor (IGF-1) analog with a binding affinity  
 CC preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1  
 CC analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a  
 CC IGFBP displacer peptide that prevents the interaction of IGF with an  
 CC IGFBP and does not bind to human IGF receptor. The method is useful for  
 CC treating cartilage disorders (CD), including degenerative CD, articular  
 CC CD such as rheumatoid arthritis and osteoarthritis. The present sequence  
 CC is human proinsulin, which was used to illustrate the invention  
 XX  
 SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 5; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 FVNQHLGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||

RESULT 6

ADC64463

ID ADC64463 standard; protein; 86 AA.

XX

AC ADC64463;

XX

DT 18-DEC-2003 (first entry)

XX

DE Amino acid sequence for human proinsulin.

XX

KW Immunoassay; human C-peptide; HCP; immune complex; human; proinsulin.

XX

OS Homo sapiens.

XX

PN US2002160435-A1.

XX

PD 31-OCT-2002.

XX

PF 12-JUN-2001; 2001US-00878380.

XX

PR 12-JUN-2000; 2000JP-00174691.

XX

PA (KITA/) KITAJIMA S.

PA (KURA/) KURANO Y.

PA (NAKA/) NAKATSUBO K.

PA (NISH/) NISHIZONO I.

XX

PI Kitajima S, Kurano Y, Nakatsubo K, Nishizono I;

XX

DR WPI; 2003-765139/72.

XX

PT Measuring human C-peptide, by reacting sample C-peptide with two  
PT different human C-peptide antibodies that recognize different epitopes on  
PT peptide, to form immune complex, separating and quantifying immune  
PT complex.

XX

PS Disclosure; SEQ ID NO 1; 20pp; English.

XX

CC The present invention relates to an immunoassay for measuring human C-  
CC peptide (HCP). The method comprises reacting HCP in a sample with a first  
CC anti-HCP antibody and a second anti-HCP antibody which is immobilised on  
CC a support, to form an immune complex, and separating and quantifying the  
CC immune complex, where the first and second antibody recognises the  
CC epitope existing in the region from 1-110 and 1-16 amino acid residues,  
CC respectively, from the N-terminal end of HCP. Also disclosed is a kit for  
CC measuring human C-peptide. The method is useful for measuring human C-  
CC peptides. The method provides high reproducibility, high detection  
CC sensitivity, and low cross-reactivity to proinsulin. The present sequence  
CC represents the amino acid sequence for human proinsulin.

XX

SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 7; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.5e-43;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy     61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db     61 SLQKRGIVEQCCTSICSLYQLENYCN 86
```

RESULT 7

ADF16632

ID ADF16632 standard; protein; 86 AA.

XX

AC ADF16632;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human albumin fusion protein-related protein SeqID1734.

XX

KW albumin fusion protein; albumin activity; human serum albumin;

KW serum osmotic pressure; shelf-life; stability; antidiabetic;

KW gene therapy; diabetes mellitus; human; gene; ds.

XX

OS Homo sapiens.

XX

PN WO2003060071-A2.

XX

PD 24-JUL-2003.

XX

PF 23-DEC-2002; 2002WO-US040891.

XX

PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0383123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411426P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (DELZ ) DELTA BIOTECHNOLOGY LTD.

PA (PRIN-) PRINCIPIA PHARM CORP.  
 XX  
 PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;  
 XX  
 DR WPI; 2003-598517/56.  
 DR N-PSDB; ADF16306.  
 XX  
 PT New albumin fusion protein, useful for preparing a composition for  
 PT treating diabetes mellitus.  
 XX  
 PS Example 4; SEQ ID NO 1734; 24pp; English.  
 XX  
 CC This invention relates to a novel albumin fusion protein having albumin  
 CC or biological activity. Human serum albumin is responsible for a  
 CC significant proportion of the osmotic pressure of serum and also  
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of  
 CC albumin to a therapeutic protein may increase shelf-life and stability of  
 CC the therapeutic protein. The albumin fusion protein of the invention may  
 CC allow production of compositions with antidiabetic activity whilst the  
 CC nucleotide sequence which encodes it may be useful for gene therapy. The  
 CC albumin fusion protein is useful for preparing a composition for treating  
 CC diabetes mellitus. The present sequence is that of a therapeutic protein  
 CC which was fused with human albumin to create a novel albumin fusion  
 CC protein of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 7; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||  
 Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

# RESULT 8

ADH21860

ID ADH21860 standard; protein; 86 AA.

XX

AC ADH21860;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human long-acting insulin peptide, SEQ ID NO:657.

XX

KW Fusion protein; human serum albumin; HSA; therapeutic protein;  
 KW shelf-life; in vitro biological activity; in vivo biological activity;  
 KW metabolic disorder; endocrine disorder; diabetes; type 1; type 2;  
 KW diabetes-related condition; hyperglycaemia; neural disorder; neuropathy;  
 KW retinopathy; cardiovascular disorder; heart disease; renal disorder;

KW obesity; glucose level maintenance; weight loss; antidiabetic; cardiant;  
 KW anorectic; ophthalmological; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003059934-A2.  
 XX  
 PD 24-JUL-2003.  
 XX  
 PF 23-DEC-2002; 2002WO-US040892.  
 XX  
 PR 21-DEC-2001; 2001US-0341811P.  
 PR 24-JAN-2002; 2002US-0350358P.  
 PR 26-FEB-2002; 2002US-0359370P.  
 PR 28-FEB-2002; 2002US-0360000P.  
 PR 27-MAR-2002; 2002US-0367500P.  
 PR 08-APR-2002; 2002US-0370227P.  
 PR 10-MAY-2002; 2002US-0378950P.  
 PR 24-JUL-2002; 2002US-0398008P.  
 PR 09-AUG-2002; 2002US-0402131P.  
 PR 13-AUG-2002; 2002US-0402708P.  
 PR 18-SEP-2002; 2002US-0411355P.  
 PR 02-OCT-2002; 2002US-0414984P.  
 PR 11-OCT-2002; 2002US-0417611P.  
 PR 23-OCT-2002; 2002US-0420246P.  
 PR 05-NOV-2002; 2002US-0423623P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Haseltine WA;  
 XX  
 DR WPI; 2003-598501/56.  
 DR N-PSDB; ADH21708.  
 XX  
 PT New albumin fusion protein, useful for preparing a composition for  
 PT treating diabetes mellitus.  
 XX  
 PS Disclosure; SEQ ID NO 657; 1086pp; English.  
 XX  
 CC The invention relates to fusion proteins comprising human serum albumin  
 CC (ADH21530) and a therapeutic polypeptide such as a therapeutic protein,  
 CC antibody or peptide or their variants or fragments. The therapeutic  
 CC protein may be fused to the N-terminus, the C-terminus or both termini of  
 CC albumin via a linker. The albumin component of the fusion proteins  
 CC prolongs the shelf-life and the in vitro and vivo biological activity of  
 CC the proteins compared with those of the corresponding therapeutic  
 CC proteins on their own. The invention also relates to nucleic acids  
 CC encoding albumin fusion proteins, vectors and host cells comprising an  
 CC albumin fusion protein nucleic acid, compositions and kits comprising an  
 CC albumin fusion protein, the method of extending the shelf-life of a  
 CC therapeutic protein by fusion with albumin, and the treatment of disease  
 CC using an albumin fusion protein. The albumin fusion proteins may be used  
 CC in the treatment of metabolic/endocrine disorders, diabetes and diabetes-  
 CC related conditions. Specifically the albumin fusion proteins may be used  
 CC to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders  
 CC (especially neuropathy), retinopathy, cardiovascular disorders  
 CC (especially heart disease, renal disorders and obesity. The proteins may



CC also be used in a method of maintaining a basal glucose level in a  
CC patient and in a method for losing weight. The present sequence is  
CC related to the invention.

XX

SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 7; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|||||

Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|||||

Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

# RESULT 9

ADT93277

ID ADT93277 standard; protein; 86 AA.

XX

AC ADT93277;

XX

DT 16-DEC-2004 (first entry)

XX

DE Human native proinsulin protein.

XX

KW antidiabetic; nephrotropic; cardiovascular; hepatotropic; anabolic;

KW gene therapy; insulin-like growth factor-I; IGF-I; dysregulation;

KW GH/IGF axis; hyperglycemic disorder; renal disorder;

KW congestive heart failure; hepatic failure; poor nutrition;

KW wasting syndrome; catabolic state; IGF binding protein-1; IGFBP-1;

KW renal failure; proinsulin.

XX

OS Homo sapiens.

XX

PN AU2003236454-A1.

XX

PD 18-SEP-2003.

XX

PF 22-AUG-2003; 2003AU-00236454.

XX

PR 22-AUG-2003; 2003AU-00236454.

XX

PA (GETH ) GENENTECH INC.

XX

PI Mortensen DL, Lowman HB, Fielder PJ, Dubaquié Y;

XX

DR WPI; 2004-662617/65.

XX

PT New insulin-like growth factor-I (IGF-I) variant, useful for treating

PT disorder associated with dysregulation of GH(growth hormone)/IGF axis

PT e.g. renal disorder.

XX

PS Disclosure; SEQ ID NO 2; 61pp; English.

XX  
 CC The invention relates to an insulin-like growth factor-I (IGF-I) variant  
 CC (I), where the amino acid residue at position 16 of native-sequence human  
 CC IGF-I is replaced with glycine or a serine residue. (I) is useful for  
 CC treating a disorder associated with dysregulation of the GH/IGF axis in a  
 CC mammal, preferably human, and for the manufacture of a medicament useful  
 CC in the treatment method. The treatment method involves administering to  
 CC the mammal an effective amount of (I). The disorder is a hyperglycemic  
 CC disorder, a renal disorder, congestive heart failure, hepatic failure,  
 CC poor nutrition, a wasting syndrome, or a catabolic state, where IGF  
 CC binding protein-1 (IGFBP-1) levels are increased relative to such levels  
 CC in a mammal without such disorder. The disorder is renal disorder. The  
 CC renal disorder is chronic or acute renal failure. The method further  
 CC involves administering an effective amount of a renally active molecule  
 CC to the mammal. (I) is useful for mapping the functional binding site for  
 CC IGF receptor. This sequence corresponds to the native human proinsulin  
 CC used as a comparison for the IGF-I used to generate the variants of the  
 CC invention.  
 XX  
 SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 8; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||||||||||  
 Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 10  
 AAP20036  
 ID AAP20036 standard; protein; 87 AA.  
 XX  
 AC AAP20036;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-JUL-1992 (first entry)  
 XX  
 DE Human proinsulin.  
 XX  
 KW Proinsulin.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP55942-A.  
 XX  
 PD 14-JUL-1982.  
 XX  
 PF 31-DEC-1981; 81EP-00306190.  
 XX  
 PR 02-JAN-1981; 81US-00222010.  
 PR 23-JUL-1981; 81US-00286070.

PR 02-JAN-1982; 82US-00222010.  
 PR 03-MAR-1982; 82US-00354287.  
 XX  
 PA (UYNY-) STATE UNIV NEW YORK.  
 XX  
 PI Inouye M, Nakamura K;  
 XX  
 DR WPI; 1982-59775E/29.  
 DR N-PSDB; AAN20041.  
 XX  
 PT Plasmid cloning vehicles - useful for transforming bacterial hosts to  
 PT produce eukaryotic polypeptide(s).  
 XX  
 PS Disclosure; Fig 27; 114pp; English.  
 XX  
 CC The sequence comprises human proinsulin. (Updated on 25-MAR-2003 to  
 CC correct PR field.)  
 XX  
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||||||||||  
 Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

RESULT 11  
 AAP40217

ID AAP40217 standard; protein; 87 AA.  
 XX  
 AC AAP40217;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-FEB-1992 (first entry)  
 XX  
 DE Sequence of the 32 N-terminal AAs of proinsulin.  
 XX  
 KW Hormone; cloning vector; phage resistant.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 2. .31  
 FT /label= B-chain  
 FT Region 32. .66  
 FT /label= C-chain  
 FT Region 67. .87  
 FT /label= A-chain  
 XX  
 PN GB2126237-A.

XX  
 PD 21-MAR-1984.  
 XX  
 PF 01-SEP-1983; 83GB-00023468.  
 XX  
 PR 03-SEP-1982; 82US-00414290.  
 PR 05-SEP-1984; 84US-00647338.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Hershberge CL, Rosteck PR;  
 XX  
 DR WPI; 1984-070793/12.  
 DR N-PSDB; AAN40179.  
 XX  
 PT Protecting bacteria from phage infection - by transformation with cloning  
 PT vector contg. segment with restriction and modification activity.  
 XX  
 PS Example; Fig 10; 28pp; English.  
 XX  
 CC Plasmid pTh alpha 1 was constructed by inserting a synthesised gene for  
 CC thymosin alpha 1 (AAN40178) into plasmid pBR322. It is used for the  
 CC construction of pTrp24. The inventors claim a method for protecting  
 CC bacteria from phage infection - by transformation with cloning vector  
 CC contg. segment with restriction and modification activity. Prodn. of  
 CC plasmid pPR 26 or pPR27 which uses pTrp24; and prodn. of plasmid pPR29  
 CC which uses a synthetic gene coding for the 32 N-terminal AAs of  
 CC proinsulin (see AAN40179). (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61  
  
 QY 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||  
 Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

# RESULT 12

AAP50127

ID AAP50127 standard; protein; 87 AA.

XX

AC AAP50127;

XX

DT 25-MAR-2003 (revised)

DT 16-AUG-2002 (revised)

DT 30-SEP-1991 (first entry)

XX

DE Sequence of the 32 N-terminal AAs of proinsulin.

XX

KW Selectable vector; autonomously replicating vector; expression vector.

XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 2. .31  
 FT /label= A chain  
 FT Region 32. .66  
 FT /label= B chain  
 FT Region 67. .87  
 FT /label= A chain  
 XX  
 PN EP154539-A.  
 XX  
 PD 11-SEP-1985.  
 XX  
 PF 04-MAR-1985; 85EP-00301469.  
 XX  
 PR 06-MAR-1984; 84US-00586592.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Schoner R, Schoner B;  
 XX  
 DR WPI; 1985-224921/37.  
 DR N-PSDB; AAN50152.  
 XX  
 PT New recombinant DNA expression vector - with autonomous replication and  
 PT on transcription generating polycistronic mrna.  
 XX  
 PS Example; Fig 14; 118pp; English.  
 XX  
 CC The inventors claim a process for preparing selectable and autonomously  
 CC replicating recombinant DNA expression vectors which comprise 1) a  
 CC transcriptional and translational activating sequence which is in the  
 CC reading frame of a nucleotide sequence which codes for a peptide or  
 CC polypeptide; 2) a translational stop signal; 3) a translational start  
 CC signal which is in the reading frame of a nucleotide sequence that codes  
 CC for a functional polypeptide; and 4) an additional translational stop  
 CC signal. The peptide or polypeptide coding sequence codes for 2-20 AAs,  
 CC esp. AAP50122-P50125. The functional polypeptide is esp. growth hormone,  
 CC human insulin, interferon and human tissue plasminogen activator.  
 CC (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003  
 CC to correct PA field.)  
 XX  
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||

RESULT 13

AAP50060

ID AAP50060 standard; protein; 87 AA.

XX

AC AAP50060;

XX

DT 25-MAR-2003 (revised)

DT 16-AUG-2002 (revised)

DT 11-NOV-1991 (first entry)

XX

DE Synthetic proinsulin.

XX

KW Proinsulin; vector; proteinaceous granule.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	1. .30
----	--------	--------

FT		/label= B chain.
----	--	------------------

FT	Region	31. .65
----	--------	---------

FT		/label= C chain.
----	--	------------------

FT	Region	66. .86
----	--------	---------

FT		/label= A chain.
----	--	------------------

XX

PN EP159123-A.

XX

PD 23-OCT-1985.

XX

PF 04-MAR-1985; 85EP-00301468.

XX

PR 06-MAR-1984; 84US-00586582.

PR 26-JUL-1984; 84US-00634920.

PR 31-JAN-1985; 85US-00697090.

XX

PA (ELIL ) LILLY & CO.ELI.

XX

PI Hsiung HM, Schoner RG, Schoner BE;

XX

DR WPI; 1985-265090/43.

DR N-PSDB; AAN50082.

XX

PT New selectable and autonomously replicating DNA expression vector -  
 PT useful in producing proteinaceous granules in cell transformants, esp.  
 PT for prodn. of bovine growth hormone derivs.

XX

PS Disclosure; Fig 14; 115pp; English.

XX

CC The synthetic proinsulin gene is expressed in a new selectable and  
 CC autonomously replicating recombinant DNA expression vector comprising a  
 CC runaway replicon and a transcriptional and translational activating  
 CC sequence in the reading frame of the proinsulin coding sequence, the  
 CC sequence contg. a translational stop signal. Host cells contg. the  
 CC vector, which is esp. plasmid pCZ103, are cultured, and proinsulin is  
 CC produced as a highly homogeneous species of proteinaceous granule. The

CC granule can be readily isolated from cell lysates and is stable on  
CC washing with urea or detergent solns. at low concns. The granule contains  
CC at least 50% of proinsulin and all isolation operations are simplified.  
CC (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003  
CC to correct PA field.)

XX

SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;  
Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|

Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|

Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

#### RESULT 14

AAP61090

ID AAP61090 standard; protein; 87 AA.

XX

AC AAP61090;

XX

DT 28-FEB-1992 (first entry)

XX

DE Sequence encoded by the structural gene for human proinsulin.

XX

KW Recombinant plasmid; E.coli expression vector; secretion vector.

XX

OS Homo sapiens.

XX

PN US4624926-A.

XX

PD 25-NOV-1986.

XX

PF 03-MAR-1982; 82US-00354287.

XX

PR 02-JAN-1981; 81US-00222010.

PR 23-JUL-1981; 81US-00286070.

XX

PA (UYNY-) UNIV OF NEW YORK.

XX

PI Inouye M, Nakamura K;

XX

DR WPI; 1986-331802/50.

DR N-PSDB; AAN60872.

XX

PT New recombinant plasmid(s) - contg. DNA sequences encoding exogenous  
PT polypeptide and outer membrane protein of E coli.

XX

PS Example; Fig 27; 44pp; English.

XX

CC The inventors claim new recombinant plasmids contg. a DNA sequence

CC encoding a polypeptide, which is foreign to E.coli, in reading phase with  
CC a DNA SQ, coding for at least one functional fragment derived from an  
CC outer membrane lipoprotein gene of E.coli. The foreign gene may be for  
CC human insulin. The lipoprotein gene functional fragment may be the  
CC promoter, the 5'-UTR, the 3'-UTR or the transcription termination signal  
CC provided that it includes at least the promoter

XX

SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;

Best Local Similarity 100.0%; Pred. No. 1.5e-43;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|||||

Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|||||

Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

#### RESULT 15

AAR32367

ID AAR32367 standard; protein; 87 AA.

XX

AC AAR32367;

XX

DT 25-MAR-2003 (revised)

DT 18-JUN-1993 (first entry)

XX

DE Proinsulin protein sequence.

XX

KW Human; proinsulin; vector; pUC19; pPINS; CAT; pUC-CAT-proinsulin;

KW insulin analogue; type I; type II; diabetes.

XX

OS Synthetic.

XX

PN WO9303174-A1.

XX

PD 18-FEB-1993.

XX

PF 31-JUL-1992; 92WO-US006451.

XX

PR 08-AUG-1991; 91US-00741938.

PR 30-JUL-1992; 92US-00918953.

XX

PA (SCIO-) SCIOS INC.

PA (PFIZ ) PFIZER INC.

XX

PI Andy RJ, Larson ER;

XX

DR WPI; 1993-076530/09.

DR N-PSDB; AAQ37003.

XX

PT New hepato selective and peripheral selective human insulin analogues -

PT and their corresp. DNA, for treatment of type I and type II diabetes.



XX  
 PS Disclosure; Fig 2b; 58pp; English.  
 XX  
 CC This sequence represents human proinsulin and was decoded from the  
 CC sequences given in AAQ36996-7001. The cDNA fragment coding for proinsulin  
 CC was inserted into plasmid vector pUC19 and digested with KpnI and  
 CC HindIII. This resulted in the formation of the vector pPINS. A fragment  
 CC encoding amino acids 1-73 of CAT (see AAQ37002) was inserted into pPINS  
 CC to give a plasmid which contained DNA sequences which coded for amino  
 CC acids 1-73 of CAT, an 8 amino acid linker sequence and human proinsulin.  
 CC This plasmid, pUC-CAT-proinsulin, could be used in the formation of  
 CC insulin analogues which may be used in the treatment of types I and II  
 CC diabetes. (Updated on 25-MAR-2003 to correct PN field.)

XX  
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 2; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG	60
Db	2	FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG	61
Qy	61	SLQKRGIVEQCCTSICSLYQLENYCN	86
Db	62	SLQKRGIVEQCCTSICSLYQLENYCN	87

Search completed: February 11, 2005, 18:14:51  
 Job time : 92.0148 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 18:04:56 ; Search time 22.69 Seconds  
(without alignments)  
282.936 Million cell updates/sec

Title: US-10-054-873-4  
Perfect score: 463  
Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	463	100.0	86	4	US-09-477-924-2	Sequence 2, Appli
2	463	100.0	86	4	US-09-723-981-2	Sequence 2, Appli
3	463	100.0	86	4	US-09-723-896-2	Sequence 2, Appli
4	463	100.0	86	4	US-09-878-380-1	Sequence 1, Appli
5	463	100.0	96	2	US-09-134-836-4	Sequence 4, Appli
6	463	100.0	96	3	US-09-386-303A-4	Sequence 4, Appli
7	463	100.0	96	4	US-09-947-563-4	Sequence 4, Appli
8	463	100.0	97	1	US-08-160-376A-4	Sequence 4, Appli
9	463	100.0	110	3	US-08-950-720A-11	Sequence 11, Appli
10	463	100.0	110	3	US-08-589-028-2	Sequence 2, Appli
11	463	100.0	110	3	US-08-784-582-2	Sequence 2, Appli

12	463	100.0	110	3	US-08-785-271-2	Sequence 2, Appli
13	463	100.0	110	4	US-08-472-701-2	Sequence 2, Appli
14	463	100.0	110	4	US-09-185-852-2	Sequence 2, Appli
15	463	100.0	110	4	US-09-815-229-3	Sequence 3, Appli
16	463	100.0	110	4	US-09-617-389B-20	Sequence 20, Appl
17	463	100.0	110	4	US-09-323-738-2	Sequence 2, Appli
18	463	100.0	110	4	US-09-015-399-7	Sequence 7, Appli
19	463	100.0	110	5	PCT-US95-08596-2	Sequence 2, Appli
20	463	100.0	117	4	US-09-280-030-63	Sequence 63, Appl
21	463	100.0	130	4	US-09-280-030-62	Sequence 62, Appl
22	463	100.0	151	2	US-08-508-664-15	Sequence 15, Appl
23	463	100.0	161	2	US-08-508-664-16	Sequence 16, Appl
24	463	100.0	167	1	US-07-918-953-8	Sequence 8, Appli
25	463	100.0	167	1	US-08-081-661-8	Sequence 8, Appli
26	457	98.7	96	2	US-09-134-836-5	Sequence 5, Appli
27	457	98.7	96	3	US-09-386-303A-5	Sequence 5, Appli
28	457	98.7	96	4	US-09-947-563-5	Sequence 5, Appli
29	457	98.7	97	1	US-08-389-487-7	Sequence 7, Appli
30	456	98.5	90	1	US-08-030-731A-43	Sequence 43, Appl
31	456	98.5	98	4	US-09-701-968-7	Sequence 7, Appli
32	456	98.5	99	4	US-09-701-968-8	Sequence 8, Appli
33	456	98.5	100	4	US-09-701-968-9	Sequence 9, Appli
34	449	97.0	110	4	US-09-574-443-1	Sequence 1, Appli
35	446	96.3	97	3	US-09-099-307-6	Sequence 6, Appli
36	444	95.9	97	3	US-09-099-307-8	Sequence 8, Appli
37	443	95.7	110	3	US-08-589-028-4	Sequence 4, Appli
38	443	95.7	110	3	US-08-784-582-4	Sequence 4, Appli
39	443	95.7	110	3	US-08-785-271-4	Sequence 4, Appli
40	440	95.0	97	3	US-09-099-307-7	Sequence 7, Appli
41	435	94.0	97	3	US-09-099-307-11	Sequence 11, Appl
42	398	86.0	91	4	US-09-676-787-7	Sequence 7, Appli
43	300	64.8	56	4	US-09-815-229-10	Sequence 10, Appl
44	292.5	63.2	67	3	US-08-981-988A-1	Sequence 1, Appli
45	290.5	62.7	83	3	US-08-981-988A-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
 US-09-477-924-2  
 ; Sequence 2, Application US/09477924  
 ; Patent No. 6403764  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dubaquie, Yves  
 ; APPLICANT: Lowman, Henry  
 ; TITLE OF INVENTION: PROTEIN VARIANTS  
 ; FILE REFERENCE: P1712R1-1  
 ; CURRENT APPLICATION NUMBER: US/09/477,924  
 ; CURRENT FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SEQ ID NO 2  
 ; LENGTH: 86  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-477-924-2

Query Match 100.0%; Score 463; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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RESULT 2

US-09-723-981-2  
; Sequence 2, Application US/09723981  
; Patent No. 6506874  
; GENERAL INFORMATION:  
; APPLICANT: Dubaquier, Yves  
; APPLICANT: Lowman, Henry  
; TITLE OF INVENTION: PROTEIN VARIANTS  
; FILE REFERENCE: P1712R1  
; CURRENT APPLICATION NUMBER: US/09/723,981  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/477,923  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 2  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-723-981-2

Query Match 100.0%; Score 463; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          ||||||||||||||||||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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RESULT 3

US-09-723-896-2  
; Sequence 2, Application US/09723896  
; Patent No. 6509443  
; GENERAL INFORMATION:  
; APPLICANT: Dubaquier, Yves  
; APPLICANT: Lowman, Henry  
; TITLE OF INVENTION: PROTEIN VARIANTS  
; FILE REFERENCE: P1712R1  
; CURRENT APPLICATION NUMBER: US/09/723,896  
; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/477,923  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 2  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-723-896-2

Query Match 100.0%; Score 463; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|  
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

#### RESULT 4

US-09-878-380-1

; Sequence 1, Application US/09878380  
; Patent No. 6534281  
; GENERAL INFORMATION:  
; APPLICANT: Fujirebio Inc.  
; APPLICANT: KITAJIMA, Sachiko  
; APPLICANT: KURANO, Yoshihiro  
; APPLICANT: NAKATSUBO, Kaoru  
; APPLICANT: NISHIZONO, Isao  
; TITLE OF INVENTION: Immunoassay For Measuring Human C-Peptide and Kit  
Therefor  
; FILE REFERENCE: 0760-0291P  
; CURRENT APPLICATION NUMBER: US/09/878,380  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: JP 2000-174691  
; PRIOR FILING DATE: 2000-06-12  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-878-380-1

Query Match 100.0%; Score 463; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.4e-47;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|  
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|

Db

61 SLQKRGIVEQCCTSIQSLYQLENYCN 86

RESULT 5

US-09-134-836-4

; Sequence 4, Application US/09134836

; Patent No. 5986048

; GENERAL INFORMATION:

; APPLICANT: Rubroder, Franz-Josef

; APPLICANT: Keller, Reinhold

; TITLE OF INVENTION: Improved process for obtaining

; TITLE OF INVENTION: insulin precursors having correctly bonded cystine  
bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farrahaw, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/134,836

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Leslie McDonell

; REGISTRATION NUMBER: 34,872

; REFERENCE/DOCKET NUMBER: 02481.1600-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 96 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..96

US-09-134-836-4

Query Match 100.0%; Score 463; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 2.8e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

```

Db      11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 70
Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
Db      71 SLQKRGIVEQCCTSICSLYQLENYCN 96

```

RESULT 6

US-09-386-303A-4

; Sequence 4, Application US/09386303A

; Patent No. 6380355

; GENERAL INFORMATION:

; APPLICANT: Rubroder, Franz-Josef

; Keller, Reinhold

; TITLE OF INVENTION: Improved process for obtaining

; insulin precursors having correctly bonded cystine

bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farrahaw, Garrett &  
; Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/386,303A

; FILING DATE: 31-Aug-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/134,836

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Leslie McDonell

; REGISTRATION NUMBER: 34,872

; REFERENCE/DOCKET NUMBER: 02481.1600-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 96 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..96  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-386-303A-4

Query Match 100.0%; Score 463; DB 3; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.8e-47;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|  
Db 11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 70  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 71 SLQKRGIVEQCCTSICSLYQLENYCN 96

RESULT 7

US-09-947-563-4  
; Sequence 4, Application US/09947563  
; Patent No. 6727346  
; GENERAL INFORMATION:  
; APPLICANT: Rubroder, Franz-Josef  
; Keller, Reinhold  
; TITLE OF INVENTION: Improved process for obtaining  
; insulin precursors having correctly bonded cystine  
bridges  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farrahaw, Garrett &  
; Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/947,563  
; FILING DATE: 07-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/134,836  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leslie McDonell  
; REGISTRATION NUMBER: 34,872  
; REFERENCE/DOCKET NUMBER: 02481.1600-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:



```

;           LENGTH: 96 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;           MOLECULE TYPE: protein
;           ORIGINAL SOURCE:
;             ORGANISM: Escherichia coli
;           FEATURE:
;             NAME/KEY: Protein
;             LOCATION: 1..96
;           SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-563-4

```

```

Query Match          100.0%; Score 463; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 70

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||||||||||
Db      71 SLQKRGIVEQCCTSICSLYQLENYCN 96

```

```

RESULT 8
US-08-160-376A-4
; Sequence 4, Application US/08160376A
; Patent No. 5473049
; GENERAL INFORMATION:
;   APPLICANT: Obermeier, Ranier
;   APPLICANT: Gerl, Martin
;   APPLICANT: Ludwig, Jurgen
;   APPLICANT: Sabel, Walter
;   TITLE OF INVENTION: Process For Obtaining Proinsulin
;   TITLE OF INVENTION: Possessing Correctly Linked
;   TITLE OF INVENTION: Cystine Bridges
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Kenneth A. Genoni, Esq.
;     STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
;     CITY: Somerville
;     STATE: New Jersey
;     COUNTRY: U.S.A.
;     ZIP: 08876-1258
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;     COMPUTER: IBM 386
;     OPERATING SYSTEM: WINDOWS 3.1
;     SOFTWARE: WORDPERFECT 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/160,376A
;     FILING DATE: December 1, 1993
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GE P 4240420.7

```

```

; FILING DATE: December 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara V. Maurer, Esq.
; REGISTRATION NUMBER: 31,287
; REFERENCE/DOCKET NUMBER: HOE 92/F 384
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 231-4079
; TELEFAX: (908) 231-2255
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 Amino Acids
; TYPE: Amino Acid (AA)
; TOPOLOGY: not relevant
US-08-160-376A-4

```

```

Query Match          100.0%; Score 463; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 71

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||||||
Db      72 SLQKRGIVEQCCTSICSLYQLENYCN 97

```

# RESULT 9

US-08-950-720A-11

; Sequence 11, Application US/08950720A

; Patent No. 6046028

## ; GENERAL INFORMATION:

; APPLICANT: Conklin, Darrell C.

; APPLICANT: Lofton-Day, Catherine E.

; APPLICANT: Lok, Si

; APPLICANT: Jaspers, Stephen R.

; TITLE OF INVENTION: INSULIN HOMOLOG

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/950,720A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
US-08-950-720A-11

```

```

Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps .0;

```

```

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          ||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

```

# RESULT 10

US-08-589-028-2

; Sequence 2, Application US/08589028

; Patent No. 6087129

; GENERAL INFORMATION:

; APPLICANT: Newgard, Christopher B.

; APPLICANT: Halban, Philippe

; APPLICANT: No. 6087129mington, Karl D.

; APPLICANT: Clark, Samuel A.

; APPLICANT: Thigpen, Anice E.

; APPLICANT: Quaade, Christian

; APPLICANT: Kruse, Fred

; TITLE OF INVENTION: Recombinant Expression of Proteins From

; TITLE OF INVENTION: Secretory Cell Lines

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,028
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 47,642
; REFERENCE/DOCKET NUMBER: UTSD:426\HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-589-028-2
```

```
Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches   86; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
```

```
Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
```

RESULT 11

US-08-784-582-2

```
; Sequence 2, Application US/08784582
; Patent No. 6110707
; GENERAL INFORMATION:
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Halban, Philippe A.
; APPLICANT: No. 6110707mington, Karl D.
; APPLICANT: Clark, Samuel A.
; APPLICANT: Thigpen, Anice E.
; APPLICANT: Quaade, Christian
; APPLICANT: Kruse, Fred
; APPLICANT: McGarry, Dennis
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
; TITLE OF INVENTION: SECRETORY CELL LINES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,582
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,427
; FILING DATE: 15-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/589,028
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:514
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-784-582-2

```

```

Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

```

RESULT 12

US-08-785-271-2

; Sequence 2, Application US/08785271

; Patent No. 6194176

; GENERAL INFORMATION:

; APPLICANT: Newgard, Christopher B.

; APPLICANT: Halban, Philippe A.

; APPLICANT: No. 6194176mington, Karl D.

; APPLICANT: Clark, Samuel A.

; APPLICANT: Thigpen, Anice E.

; APPLICANT: Quaade, Christian

; APPLICANT: Kruse, Fred

; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM

; TITLE OF INVENTION: SECRETORY CELL LINES

; NUMBER OF SEQUENCES: 56

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,271
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/589,028
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:513
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-785-271-2

```

```

Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

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RESULT 13

US-08-472-701-2

```

; Sequence 2, Application US/08472701
; Patent No. 6509165
; GENERAL INFORMATION:
; APPLICANT: Griffin, Ann C.
; APPLICANT: Hickey, William F.
; TITLE OF INVENTION: Detection and Treatment Methods for
; TITLE OF INVENTION: Type I Diabetes
; NUMBER OF SEQUENCES: 23

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,701
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,220
; FILING DATE: 08-JULY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: DCI-092DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-701-2

```

```

Query Match          100.0%;  Score 463;  DB 4;  Length 110;
Best Local Similarity 100.0%;  Pred. No. 3.3e-47;
Matches    86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

QY      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

QY      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

```

```

RESULT 14
US-09-185-852-2
; Sequence 2, Application US/09185852
; Patent No. 6537806
; GENERAL INFORMATION:
; APPLICANT: Osborne, William R.A.
; APPLICANT: Ramesh, Nagarajan
; TITLE OF INVENTION: Compositions and Methods for Treating Diabetes
; FILE REFERENCE: P-UW 3264

```

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; CURRENT APPLICATION NUMBER: US/09/185,852
; CURRENT FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/087,660
; EARLIER FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-185-852-2
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Query Match 100.0%; Score 463; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 3.3e-47;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        |||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
        |||
Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

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RESULT 15

US-09-815-229-3

; Sequence 3, Application US/09815229

; Patent No. 6689747

; GENERAL INFORMATION:

; APPLICANT: Filvaroff, Ellen H.

; APPLICANT: Okumu, Franklin W.

; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS

; FILE REFERENCE: P1786R1US

; CURRENT APPLICATION NUMBER: US/09/815,229

; CURRENT FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: US 60/192,103

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 3

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-815-229-3

Query Match 100.0%; Score 463; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 3.3e-47;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        |||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
        |||
Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

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Search completed: February 11, 2005, 18:27:05  
Job time : 24.69 secs

OM protein - protein search, using sw model

Run on: February 11, 2005, 17:42:33 ; Search time 16.3432 Seconds  
(without alignments)  
506.306 Million cell updates/sec

Title: US-10-054-873-4  
Perfect score: 463  
Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	463	100.0	110	1	IPHU	insulin precursor
2	463	100.0	110	2	A42179	insulin precursor
3	456	98.5	110	2	B42179	insulin precursor
4	456	98.5	110	2	JQ0178	insulin precursor
5	424	91.6	110	1	INRB	insulin precursor
6	417	90.1	110	1	IPDG	insulin precursor
7	394	85.1	86	1	IPHO	insulin precursor
8	394	85.1	110	1	INMS2	insulin 2 precurs
9	394	85.1	110	1	IPRT2	insulin 2 precurs
10	392	84.7	108	2	A39883	insulin precursor
11	392	84.7	110	2	I48166	insulin precursor
12	385	83.2	110	1	IPRT1	insulin 1 precurs
13	383	82.7	84	1	IPPG	insulin precursor

14	366.5	79.2	105	1	IPBO	insulin precursor
15	366	79.0	108	1	INMS1	insulin 1 precurs
16	334.5	72.2	108	2	S09278	insulin precursor
17	320.5	69.2	77	1	INSH	insulin precursor
18	314	67.8	110	1	IPGP	insulin precursor
19	277.5	59.9	109	1	IPRTDU	insulin precursor
20	276.5	59.7	103	2	I51221	insulin precursor
21	265.5	57.3	106	1	IPXL2	insulin II precurs
22	265.5	57.3	107	1	IPCH	insulin precursor
23	262.5	56.7	106	1	IPXL1	insulin I precurs
24	256.5	55.4	51	1	INEL	insulin - elephant
25	256.5	55.4	51	1	INWHF	insulin - finback
26	256.5	55.4	51	1	INWHP	insulin - sperm wh
27	256.5	55.4	81	1	IPDK	insulin precursor
28	256	55.3	96	2	PC7082	epidermal growth f
29	254.5	55.0	51	1	INHY	insulin - hamster
30	251.5	54.3	51	1	INMSSP	insulin - Egyptian
31	250.5	54.1	51	2	A59151	insulin precursor
32	246.5	53.2	51	1	INCMA	insulin - Arabian
33	246.5	53.2	51	1	INGT	insulin - goat
34	246.5	53.2	51	1	INWH1S	insulin - sei whal
35	245.5	53.0	51	1	INCT	insulin - cat
36	244.5	52.8	51	1	INMKSQ	insulin - common s
37	239.5	51.7	51	2	JQ0362	insulin - North Am
38	234.5	50.6	51	1	INCB	insulin - Chinchil
39	231.5	50.0	51	1	INGS	insulin - goose
40	227.5	49.1	51	1	INOS	insulin - ostrich
41	227.5	49.1	51	1	INTK	insulin - turkey (
42	227.5	49.1	51	1	A61129	insulin - black-be
43	227.5	49.1	51	1	INPQ	insulin - crested
44	227.5	49.1	51	2	A60414	insulin - slider t
45	225	48.6	52	2	S44470	insulin I2 - North

#### ALIGNMENTS

##### RESULT 1

IPHU

insulin precursor [validated] - human

N;Alternate names: preproinsulin

C;Species: Homo sapiens (man)

C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004

C;Accession: A93222; A94253; A93216; A94251; A93144; A92075; A91186; I58114; A01579; S58661

R;Bell, G.I.; Pictet, R.L.; Rutter, W.J.; Cordell, B.; Tischer, E.; Goodman, H.M.

Nature 284, 26-32, 1980

A;Title: Sequence of the human insulin gene.

A;Reference number: A93222; MUID:80120725; PMID:6243748

A;Accession: A93222

A;Molecule type: DNA

A;Residues: 1-110 <BEL>

A;Cross-references: UNIPROT:P01308; GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828

R;Ullrich, A.; Dull, T.J.; Gray, A.; Brosius, J.; Sures, I.

Science 209, 612-615, 1980

A;Title: Genetic variation in the human insulin gene.  
 A;Reference number: A94253; MUID:80236313; PMID:6248962  
 A;Accession: A94253  
 A;Molecule type: DNA  
 A;Residues: 1-110 <ULL>  
 A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828  
 R;Bell, G.I.; Swain, W.F.; Pictet, R.; Cordell, B.; Goodman, H.M.; Rutter, W.J.  
 Nature 282, 525-527, 1979  
 A;Title: Nucleotide sequence of a cDNA clone encoding human preproinsulin.  
 A;Reference number: A93216; MUID:80054779; PMID:503234  
 A;Accession: A93216  
 A;Molecule type: mRNA  
 A;Residues: 1-110 <BEL2>  
 A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828  
 R;Sures, I.; Goeddel, D.V.; Gray, A.; Ullrich, A.  
 Science 208, 57-59, 1980  
 A;Title: Nucleotide sequence of human preproinsulin complementary DNA.  
 A;Reference number: A94251; MUID:80147417; PMID:6927840  
 A;Accession: A94251  
 A;Molecule type: mRNA  
 A;Residues: 1-110 <SUR>  
 A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828  
 R;Nicol, D.S.H.W.; Smith, L.F.  
 Nature 187, 483-485, 1960  
 A;Title: Amino-acid sequence of human insulin.  
 A;Reference number: A93144  
 A;Accession: A93144  
 A;Molecule type: protein  
 A;Residues: 25-54;90-110 <NIC>  
 R;Oyer, P.E.; Cho, S.; Peterson, J.D.; Steiner, D.F.  
 J. Biol. Chem. 246, 1375-1386, 1971  
 A;Title: Studies on human proinsulin. Isolation and amino acid sequence of the human pancreatic C-peptide.  
 A;Reference number: A92075; MUID:71116410; PMID:5101771  
 A;Accession: A92075  
 A;Molecule type: protein  
 A;Residues: 57-87 <OYE>  
 R;Ko, A.; Smyth, D.G.; Markussen, J.; Sundby, F.  
 Eur. J. Biochem. 20, 190-199, 1971  
 A;Title: Amino acid sequence of the C-peptide of human proinsulin.  
 A;Reference number: A91186; MUID:71257722; PMID:5560404  
 A;Accession: A91186  
 A;Molecule type: protein  
 A;Residues: 57-87 <KOA>  
 R;Lucassen, A.M.; Julier, C.; Beressi, J.P.; Boitard, C.; Froguel, P.; Lathrop, M.; Bell, J.I.  
 Nature Genet. 4, 305-310, 1993  
 A;Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment of DNA spanning the insulin gene and associated VNTR.  
 A;Reference number: I58114; MUID:93364428; PMID:8358440  
 A;Accession: I58114  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-59,63-110 <RES>  
 A;Cross-references: GB:L15440; NID:g307071; PIDN:AAA59179.1; PID:g307072  
 R;Sieber, P.; Kamber, B.; Hartmann, A.; Joehl, A.; Riniker, B.; Rittel, W.  
 Helv. Chim. Acta 57, 2617-2621, 1974

A;Title: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindungen.  
A;Reference number: A91636; MUID:75077277; PMID:4443293  
A;Contents: annotation; synthesis  
A;Note: disulfide-bonded human insulin was synthesized; the synthetic hormone was identical with the natural hormone in chemical and biological activities  
A;Note: article in German with English abstract  
R;Naithani, V.K.  
Hoppe-Seyler's Z. Physiol. Chem. 354, 659-672, 1973  
A;Title: The synthesis of C-peptide of human proinsulin.  
A;Reference number: A91658; MUID:75040007; PMID:4803504  
A;Contents: annotation; synthesis of residues 57-87  
R;Geiger, R.; Jaeger, G.; Koenig, W.  
Chem. Ber. 106, 2347-2352, 1973  
A;Title: Synthesis of the complete sequence of human proinsulin C-peptide and its [Glu-9,Gln-11] analogue.  
A;Reference number: A90914  
A;Contents: annotation; synthesis of residues 57-87  
R;Kaufmann, J.E.; Irminger, J.C.; Halban, P.A.  
Biochem. J. 310, 869-874, 1995  
A;Title: Sequence requirements for proinsulin processing at the B-chain/C-peptide junction.  
A;Reference number: S58661; MUID:96013185; PMID:7575420  
A;Contents: annotation; site-directed mutagenesis study of proteolytic processing  
C;Genetics:  
A;Gene: GDB:INS  
A;Cross-references: GDB:119349; OMIM:176730  
A;Map position: 11p15.5-11p15.5  
A;Introns: 63/1  
C;Superfamily: insulin  
C;Keywords: hormone; pancreas  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-54/Domain: insulin chain B #status experimental <BCH>  
F;25-54,90-110/Product: insulin #status experimental <MAT>  
F;57-87/Domain: connecting C peptide #status experimental <CPEP>  
F;90-110/Domain: insulin chain A #status experimental <ACH>  
F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 100.0%; Score 463; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 6.8e-43;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

```

## RESULT 2

A42179

insulin precursor - chimpanzee

C;Species: Pan troglodytes (chimpanzee)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A42179; S22058  
 R;Seino, S.; Bell, G.I.; Li, W.H.  
 Mol. Biol. Evol. 9, 193-203, 1992  
 A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys.  
 A;Reference number: A42179; MUID:92219953; PMID:1560757  
 A;Accession: A42179  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-110 <SEI>  
 A;Cross-references: UNIPROT:P30410; EMBL:X61089; NID:g38251; PIDN:CAA43403.1; PID:g38252  
 A;Note: sequence extracted from NCBI backbone (NCBIP:95067)  
 C;Genetics:  
 A;Introns: 63/1  
 C;Superfamily: insulin

Query Match 100.0%; Score 463; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-43;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
  
```

# RESULT 3

B42179

insulin precursor - green monkey

C;Species: Cercopithecus aethiops (green monkey, grivet)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: B42179; A05232; S16494; S22056

R;Seino, S.; Bell, G.I.; Li, W.H.

Mol. Biol. Evol. 9, 193-203, 1992

A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys.

A;Reference number: A42179; MUID:92219953; PMID:1560757

A;Accession: B42179

A;Molecule type: DNA

A;Residues: 1-110 <SEI>

A;Cross-references: UNIPROT:P30407; EMBL:X61092; NID:g22808; PIDN:CAA43405.1; PID:g22809

A;Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)

R;Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.

J. Biol. Chem. 247, 4866-4871, 1972

A;Title: Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure.

A;Reference number: A92111; MUID:72258016; PMID:4626369

A;Accession: A05232

A;Molecule type: protein

A;Residues: 57-87 <PET>

C;Genetics:

A;Introns: 63/1

C;Superfamily: insulin  
C;Keywords: hormone; pancreas  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-54/Domain: insulin chain B #status predicted <BCH>  
F;25-54,90-110/Product: insulin #status predicted <MAT>  
F;57-87/Domain: connecting peptide #status experimental <CPEP>  
F;90-110/Domain: insulin chain A #status predicted <ACH>  
F;31-96,43-109,95-100/Disulfide bonds: #status predicted

Query Match 98.5%; Score 456; DB 2; Length 110;  
Best Local Similarity 98.8%; Pred. No. 3.9e-42;  
Matches 85; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          ||||||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
```

#### RESULT 4

JQ0178

insulin precursor - crab-eating macaque

C;Species: *Macaca fascicularis* (crab-eating macaque)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C;Accession: JQ0178

R;Wetekom, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.  
Gene 19, 179-183, 1982

A;Title: The nucleotide sequence of cDNA coding for preproinsulin from the  
primate *Macaca fascicularis*.

A;Reference number: JQ0178; MUID:83080474; PMID:6184262

A;Accession: JQ0178

A;Molecule type: mRNA

A;Residues: 1-110 <WET>

A;Cross-references: UNIPROT:P30406; GB:J00336; NID:g342121; PIDN:AAA36849.1;  
PID:g342122

C;Superfamily: insulin

F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-54,90-110/Product: insulin #status predicted <MAT>  
F;25-54/Domain: insulin chain B #status predicted <BCH>  
F;55-89/Domain: insulin connecting C peptide #status predicted <CPT>  
F;90-110/Domain: insulin chain A #status predicted <ACH>  
F;31-96,43-109,95-100/Disulfide bonds: #status predicted

Query Match 98.5%; Score 456; DB 2; Length 110;  
Best Local Similarity 98.8%; Pred. No. 3.9e-42;  
Matches 85; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          ||||||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
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## INRB

N;Alternate names: preproinsulin

C;Date: 24-Apr-1984 #sequence\_revision 23-Aug-1997 #text\_change 09-Jul-2004

R;Devaskar, S.U.; Giddings, S.J.; Rajakumar, P.A.; Carnaghi, L.R.; Menon, R.K.;  
Zahm, D.S.

A;Title: Insulin gene expression and insulin synthesis in mammalian neuronal cells.

A;Accession: A53438

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P01311; GB:U03610; NID:g467970; PIDN:AAA19033.1; PID:g467971

Am. J. Med. 40, 662-666, 1966

A;Reference number: A90029; MUID:66160119; PMID:5949593

A;Molecule type: protein

C;Superfamily: insulin

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-54,90-110/Product: insulin #status experimental <MAT>

F;90-110/Domain: insulin chain A #status experimental <ACH>

Query Match 91.6%; Score 424; DB 1; Length 110;

Best Local Similarity 90.7%; Pred. No. 1.1e-38;

Matches 78; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 25 FVNOHLCGSHLVEALYLVCGERGFFYTPKSRREVEELQVGQAELGGGPGAGGLQPSALEL 84

: | | | | | | | | | | | | | | | | | | | |

Db 85 ALQKRGIVEQCCTSICSLYQLENYCN 110

## IPDG

C;Species: Canis lupus familiaris (dog)

C:\Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004

C;Accession: A92413; A01587; S16493

R; Kwok, S.C.M.; Chan, S.J.; Steiner, D.F.



A;Reference number: A90082

A;Accession: A01580  
 A;Molecule type: protein  
 A;Residues: 1-30;66-86 <HAR>  
 A;Cross-references: UNIPROT:P01310  
 R;Tager, H.S.; Steiner, D.F.  
 J. Biol. Chem. 247, 7936-7940, 1972  
 A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.  
 A;Reference number: A92120; MUID:73061498; PMID:4640931  
 A;Accession: A92120  
 A;Molecule type: protein  
 A;Residues: 33-63 <TAG>  
 C;Comment: X's at positions 31-32 and 64-65 represent paired basic residues assumed (by homology) to be present in the precursor molecule.  
 C;Superfamily: insulin  
 C;Keywords: hormone; pancreas  
 F;1-30/Domain: insulin chain B #status experimental <BCH>  
 F;1-30,66-86/Product: insulin #status experimental <MAT>  
 F;33-63/Domain: connecting peptide #status experimental <CPEP>  
 F;66-86/Domain: insulin chain A #status experimental <ACH>  
 F;7-72,19-85,71-76/Disulfide bonds: #status predicted

Query Match 85.1%; Score 394; DB 1; Length 86;  
 Best Local Similarity 84.9%; Pred. No. 1.5e-35;  
 Matches 73; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKAXXEAEDPQVGVEVLGGGPGGLQPLALAG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |
Db      61 PQQXXGIVEQCCTGICSLYQLENYCN 86
  
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# RESULT 8

## INMS2

insulin 2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004

C;Accession: A26342; B48172; A61012; B01592

R;Wentworth, B.M.; Schaefer, I.M.; Villa-Komaroff, L.; Chirgwin, J.M.

J. Mol. Evol. 23, 305-312, 1986

A;Title: Characterization of the two nonallelic genes encoding mouse preproinsulin.

A;Reference number: A92965; MUID:87169768; PMID:3104603

A;Accession: A26342

A;Molecule type: DNA

A;Residues: 1-110 <WEN>

A;Cross-references: UNIPROT:P01326; GB:X04724; NID:g52714; PIDN:CAA28433.1; PID:g52715

R;Sawa, T.; Ohgaku, S.; Morioka, H.; Yano, S.

J. Mol. Endocrinol. 5, 61-67, 1990

A;Title: Molecular cloning and DNA sequence analysis of preproinsulin genes in the NON mouse, an animal model of human non-obese, non-insulin-dependent diabetes mellitus.

A;Reference number: A48172; MUID:90372989; PMID:2397023

A;Accession: B48172  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-110 <SAW>  
 R;Linde, S.; Nielsen, J.H.; Hansen, B.; Welinder, B.S.  
 J. Chromatogr. 462, 243-254, 1989  
 A;Title: Reversed-phase high-performance liquid chromatographic analyses of insulin biosynthesis in isolated rat and mouse islets.  
 A;Reference number: A61012; MUID:89292078; PMID:2661585  
 A;Accession: A61012  
 A;Molecule type: protein  
 A;Residues: 57-87 <LIN>  
 R;Buenzli, H.F.; Glatthaar, B.; Kunz, P.; Muelhaupt, E.; Humbel, R.E.  
 Hoppe-Seyler's Z. Physiol. Chem. 353, 451-458, 1972  
 A;Title: Amino acid sequence of the two insulins from mouse (*Mus musculus*).  
 A;Reference number: A01592; MUID:72189455; PMID:5063718  
 A;Accession: B01592  
 A;Molecule type: protein  
 A;Residues: 25-54;90-110 <BUE>  
 C;Genetics:  
 A;Introns: 63/1  
 C;Superfamily: insulin  
 C;Keywords: hormone; pancreas  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-54/Domain: insulin chain B #status experimental <BCH>  
 F;25-54,90-110/Product: insulin #status experimental <MAT>  
 F;57-87/Domain: connecting peptide #status experimental <CPEP>  
 F;90-110/Domain: insulin chain A #status experimental <ACH>  
 F;31-96,43-109,95-100/Disulfide bonds: #status predicted

Query Match 85.1%; Score 394; DB 1; Length 110;  
 Best Local Similarity 84.9%; Pred. No. 1.9e-35;  
 Matches 73; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      25 FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVEDPQVAQLLELGGGPGAGDLQTLALEV 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          : |||||:||||| ||||| |||||
Db      85 AQQKRGIVDQCCTSICSLYQLENYCN 110
  
```

# RESULT 9

IPRT2

insulin 2 precursor - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004

C;Accession: B90789; B94231; C92120; I64880; A01590; B92120

R;Lomedico, P.; Rosenthal, N.; Efstratiadis, A.; Gilbert, W.; Kolodner, R.; Tizard, R.

Cell 18, 545-558, 1979

A;Title: The structure and evolution of the two nonallelic rat preproinsulin genes.

A;Reference number: A90789; MUID:80045035; PMID:498284

A;Accession: B90789

A;Molecule type: DNA

A;Residues: 1-110 <LOM>  
 A;Cross-references: UNIPROT:P01323; GB:J00748; NID:g204958; PIDN:AAA41443.1; PID:g204959  
 R;Steiner, D.F.; Clark, J.L.; Nolan, C.; Rubenstein, A.H.; Margoliash, E.; Aten, B.; Oyer, P.E.  
 Recent Prog. Horm. Res. 25, 207-282, 1969  
 A;Title: Proinsulin and the biosynthesis of insulin.  
 A;Reference number: A94231; MUID:70067613; PMID:4311938  
 A;Accession: B94231  
 A;Molecule type: protein  
 A;Residues: 25-54;90-110 <STE>  
 R;Tager, H.S.; Steiner, D.F.  
 J. Biol. Chem. 247, 7936-7940, 1972  
 A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.  
 A;Reference number: A92120; MUID:73061498; PMID:4640931  
 A;Accession: C92120  
 A;Molecule type: protein  
 A;Residues: 57-87 <TAG>  
 R;Lomedico, P.T.; Rosenthal, N.; Kolodner, R.; Efstratiadis, A.; Gilbert, W.  
 Ann. N. Y. Acad. Sci. 343, 425-432, 1980  
 A;Title: The structure of rat preproinsulin genes.  
 A;Reference number: I51945; MUID:80240379; PMID:6249167  
 A;Accession: I64880  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-110 <RES>  
 A;Cross-references: GB:M25585; NID:g204950; PIDN:AAA41440.1; PID:g204952  
 C;Genetics:  
 A;Gene: INS2  
 A;Introns: 63/1  
 C;Superfamily: insulin  
 C;Keywords: hormone; pancreas  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-54/Domain: insulin chain B #status experimental <BCH>  
 F;25-54,90-110/Product: insulin #status experimental <MAT>  
 F;57-87/Domain: connecting peptide #status experimental <CPEP>  
 F;90-110/Domain: insulin chain A #status experimental <ACH>  
 F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 85.1%; Score 394; DB 1; Length 110;  
 Best Local Similarity 84.9%; Pred. No. 1.9e-35;  
 Matches 73; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          || |||||
Db      25 FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVDPQVAQLELGGGPGAGDLQTLALEV 84
          :||| || || |:||||| || |||
Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          : |||||:|||||
Db      85 ARQKRGIVDQCCTSICSLYQLENYCN 110
  
```

RESULT 10

A39883

insulin precursor - douroucouli

C;Species: Aotus trivirgatus (douroucouli, night monkey, owl monkey)

C;Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 09-Jul-2004  
C;Accession: A39883  
R;Seino, S.; Steiner, D.F.; Bell, G.I.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7423-7427, 1987  
A;Title: Sequence of a New World primate insulin having low biological potency  
and immunoreactivity.  
A;Reference number: A39883; MUID:88041119; PMID:3118367  
A;Accession: A39883  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-108 <SEI>  
A;Cross-references: UNIPROT:P10604; GB:J02989; NID:gl76555; PIDN:AAA35374.1;  
PID:gl76556  
C;Superfamily: insulin

RESULT 11

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Query Match          84.7%;   Score 392;   DB 2;   Length 110;
Best Local Similarity 84.9%;   Pred. No. 3.2e-35;
Matches    73;   Conservative    4;   Mismatches    9;   Indels    0;   Gaps    0;

Qy          1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
             |||||||||||||||||||||||||||||:|  || || |:|||||||  || ||||
Db          25 FVNQHLCGSHLVEALYLVCGERGFFYTPKSRRGVEDPQVAQLGEGPGADDLQTLALEV 84

Qy          61 SLQKRGIVEQCCTSICSLYQLENYCN 86
             : |||||||:|||||||||||||||||||
Db          85 AQQKRGIVDQCCTSICSLYQLENYCN 110

```

RESULT 12

IPRT1

insulin 1 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004

C;Accession: A90788; A90789; A94231; B92120; I51945; A01589

R;Cordell, B.; Bell, G.; Tischer, E.; DeNoto, F.M.; Ullrich, A.; Pictet, R.; Rutter, W.J.; Goodman, H.M.

Cell 18, 533-543, 1979

A;Title: Isolation and characterization of a cloned rat insulin gene.

A;Reference number: A90788; MUID:80045034; PMID:498283

A;Accession: A90788

A;Molecule type: DNA

A;Residues: 1-110 <COR>

A;Cross-references: UNIPROT:P01322; GB:J00747; NID:g204956; PIDN:AAA41442.1; PID:g204957

R;Lomedico, P.; Rosenthal, N.; Efstratiadis, A.; Gilbert, W.; Kolodner, R.; Tizard, R.

Cell 18, 545-558, 1979

A;Title: The structure and evolution of the two nonallelic rat preproinsulin genes.

A;Reference number: A90789; MUID:80045035; PMID:498284

A;Accession: A90789

A;Molecule type: DNA

A;Residues: 1-110 <LOM>

A;Cross-references: GB:J00747; NID:g204956; PIDN:AAA41442.1; PID:g204957

R;Steiner, D.F.; Clark, J.L.; Nolan, C.; Rubenstein, A.H.; Margoliash, E.; Aten, B.; Oyer, P.E.

Recent Prog. Horm. Res. 25, 207-282, 1969

A;Title: Proinsulin and the biosynthesis of insulin.

A;Reference number: A94231; MUID:70067613; PMID:4311938

A;Accession: A94231

A;Molecule type: protein

A;Residues: 25-54;90-110 <STE>

R;Tager, H.S.; Steiner, D.F.

J. Biol. Chem. 247, 7936-7940, 1972

A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.

A;Reference number: A92120; MUID:73061498; PMID:4640931

A;Accession: B92120

A;Molecule type: protein

A;Residues: 57-87 <TAG>

R;Lomedico, P.T.; Rosenthal, N.; Kolodner, R.; Efstratiadis, A.; Gilbert, W. Ann. N. Y. Acad. Sci. 343, 425-432, 1980

A;Title: The structure of rat preproinsulin genes.

A;Reference number: I51945; MUID:80240379; PMID:6249167

A;Accession: I51945

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-110 <RES>

A;Cross-references: GB:M25584; NID:g204947; PIDN:AAA41439.1; PID:g204948

C;Genetics:

A;Gene: INS1

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-54/Domain: insulin chain B #status experimental <BCH>  
F;25-54,90-110/Product: insulin #status experimental <MAT>  
F;57-87/Domain: connecting peptide #status experimental <CPEP>  
F;90-110/Domain: insulin chain A #status experimental <ACH>  
F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 83.2%; Score 385; DB 1; Length 110;  
Best Local Similarity 83.7%; Pred. No. 1.8e-34;  
Matches 72; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        || ||||| |||||:|||| || || |:||||| || || |||||
Db      25 FVKQHLCGPHLVEALYLVCGERGFFYTPKSRREVEDPQVPQLELGGGPEAGDLQTLALEV 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        : |||||:|||||
Db      85 ARQKRGIVDQCCTSICSLYQLENYCN 110
```

#### RESULT 13

##### IPPG

insulin precursor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 22-Jun-1981 #sequence\_revision 22-Jun-1981 #text\_change 16-Jul-1999

C;Accession: A01583; A94572; S16492; A60835; B60835

R;Chance, R.E.; Ellis, R.M.; Bromer, W.W.

Science 161, 165-167, 1968

A;Title: Porcine proinsulin: characterization and amino acid sequence.

A;Reference number: A94240; MUID:68286485; PMID:5657063

A;Accession: A01583

A;Molecule type: protein

A;Residues: 1-34, 'Q', 36-84 <CHA>

R;Chance, R.E.

submitted to the Atlas, July 1970

A;Reference number: A94572

A;Accession: A94572

A;Molecule type: protein

A;Residues: 1-84 <CH2>

R;Brown, H.; Sanger, F.; Kitai, R.

Biochem. J. 60, 556-565, 1955

A;Title: The structure of pig and sheep insulins.

A;Reference number: A90344

A;Accession: S16492

A;Molecule type: protein

A;Residues: 1-30;31-51 <BRO>

R;Snel, L.; Damgaard, U.

Horm. Metab. Res. 20, 476-480, 1988

A;Title: Proinsulin heterogeneity in pigs.

A;Reference number: A60835; MUID:89032178; PMID:3181865

A;Accession: A60835

A;Molecule type: protein

A;Residues: 33-38,40-62 <SNE>

A;Note: the authors report the characterization of a connecting peptide variant lacking Ala-39

A;Accession: B60835

A;Molecule type: protein

A;Residues: 33-62 <SN2>

F;7-70,19-83,69-74/Disulfide bonds: #status experimental

Matches 74; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

Db 59 PPQKRGIVEQCCTSI<sup>1</sup>CSLYQLENYCN 84

J. Biol. Chem. 246, 1365-1374, 1971



A;Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas.  
A;Reference number: A92074; MUID:71116409; PMID:5545080  
A;Accession: A92074  
A;Molecule type: protein  
A;Residues: 57-82 <STE>  
R;Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F.  
Eur. J. Biochem. 20, 183-189, 1971  
A;Title: Bovine proinsulin: amino acid sequence of the C-peptide isolated from pancreas.  
A;Reference number: A91185; MUID:71257721; PMID:5105368  
A;Accession: A91185  
A;Molecule type: protein  
A;Residues: 57-82 <SAL>  
R;Sanger, F.; Thompson, E.O.P.  
Biochem. J. 53, 366-374, 1953  
A;Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.  
A;Reference number: A90342  
A;Accession: A90342  
A;Molecule type: protein  
A;Residues: 85-105 <SAN>  
R;Sanger, F.; Tuppy, H.  
Biochem. J. 49, 481-490, 1951  
A;Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.  
A;Reference number: A90341  
A;Accession: A90341  
A;Molecule type: protein  
A;Residues: 25-54 <SA2>  
R;Cheng, R.; Kawakishi, S.  
Eur. J. Biochem. 223, 759-764, 1994  
A;Title: Site-specific oxidation of histidine residues in glycated insulin mediated by Cu(2+).  
A;Reference number: S48184; MUID:94333378; PMID:8055951  
A;Accession: S48184  
A;Molecule type: protein  
A;Residues: 85-105 <CHE>  
A;Accession: S48185  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 25-30,'X',32-42,'X',44-54 <CH2>  
R;Ryle, A.P.; Sanger, F.; Smith, L.F.; Kitai, R.  
Biochem. J. 60, 541-556, 1955  
A;Title: The disulphide bonds of insulin.  
A;Reference number: A90343  
A;Contents: annotation; amides; disulfides  
R;Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.  
FEBS Lett. 349, 205-209, 1994  
A;Title: Existence of a molecular ruler in proteasomes suggested by analysis of degradation products.  
A;Reference number: S46258; MUID:94326921; PMID:8050567  
A;Accession: S46258  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 25-54 <WEN>  
C;Superfamily: insulin

C;Keywords: hormone; pancreas  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-54/Domain: insulin chain B #status experimental <BCH>  
 F;25-54,85-105/Product: insulin #status experimental <MAT>  
 F;57-82/Domain: connecting peptide #status experimental <CPEP>  
 F;85-105/Domain: insulin chain A #status experimental <ACH>  
 F;31-91,43-104,90-95/Disulfide bonds: #status experimental

Query Match 79.2%; Score 366.5; DB 1; Length 105;  
 Best Local Similarity 80.2%; Pred. No. 1.7e-32;  
 Matches 69; Conservative 2; Mismatches 10; Indels 5; Gaps 1;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEGPQVGALELAGGPGAG-----GLEG 79
          |||

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      80 PPQKRGIVEQCCASVCSLYQLENYCN 105
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```

# RESULT 15

INMS1

insulin 1 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 24-Apr-1984 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004

C;Accession: B26342; A48172; A01592; B61012

R;Wentworth, B.M.; Schaefer, I.M.; Villa-Komaroff, L.; Chirgwin, J.M.

J. Mol. Evol. 23, 305-312, 1986

A;Title: Characterization of the two nonallelic genes encoding mouse preproinsulin.

A;Reference number: A92965; MUID:87169768; PMID:3104603

A;Accession: B26342

A;Molecule type: DNA

A;Residues: 1-108 <WEN>

A;Cross-references: UNIPROT:P01325; GB:X04725; NID:g52712; PIDN:CAA28434.1; PID:g52713

R;Sawa, T.; Ohgaku, S.; Morioka, H.; Yano, S.

J. Mol. Endocrinol. 5, 61-67, 1990

A;Title: Molecular cloning and DNA sequence analysis of preproinsulin genes in the NON mouse, an animal model of human non-obese, non-insulin-dependent diabetes mellitus.

A;Reference number: A48172; MUID:90372989; PMID:2397023

A;Accession: A48172

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-108 <SAW>

R;Buenzli, H.F.; Glatthaar, B.; Kunz, P.; Muelhaupt, E.; Humbel, R.E.

Hoppe-Seyler's Z. Physiol. Chem. 353, 451-458, 1972

A;Title: Amino acid sequence of the two insulins from mouse (Mus musculus).

A;Reference number: A01592; MUID:72189455; PMID:5063718

A;Accession: A01592

A;Molecule type: protein

A;Residues: 25-54;88-108 <BUE>

R;Linde, S.; Nielsen, J.H.; Hansen, B.; Welinder, B.S.

J. Chromatogr. 462, 243-254, 1989

A;Title: Reversed-phase high-performance liquid chromatographic analyses of insulin biosynthesis in isolated rat and mouse islets.

A;Reference number: A61012; MUID:89292078; PMID:2661585

A;Accession: B61012

A;Molecule type: protein

A;Residues: 57-85 <LIN>

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-54/Domain: insulin chain B #status experimental <BCH>

F;25-54,88-108/Product: insulin #status experimental <MAT>

F;57-85/Domain: connecting peptide #status experimental <CPEP>

F;88-108/Domain: insulin chain A #status experimental <ACH>

F;31-94,43-107,93-98/Disulfide bonds: #status predicted

Query Match 79.0%; Score 366; DB 1; Length 108;

Best Local Similarity 81.4%; Pred. No. 2e-32;

Matches 70; Conservative 4; Mismatches 10; Indels 2; Gaps 1;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG .60  
|| ||||| |||||||||||||||||||||:|||| || || |:|||| | | || |||||

Db 25 FVKQHLCGPHLVEALYLVCGERGFFYTPKSRREVEDPQVEQLELGGSP--GDLQTLALEV 82

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
: ||||||:|||||||||||||||||

Db 83 ARQKRGIVDQCCTSICSLYQLENYCN 108

Search completed: February 11, 2005, 18:24:35

Job time : 17.3432 secs

OM protein - protein search, using sw model

Run on: February 11, 2005, 18:23:02 ; Search time 62.5166 Seconds  
(without alignments)  
449.487 Million cell updates/sec

Title: US-10-054-873-4  
Perfect score: 463  
Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	463	100.0	86	9	US-09-878-380-1	Sequence 1, Appli
2	463	100.0	86	10	US-09-858-935B-4	Sequence 4, Appli
3	463	100.0	86	13	US-10-028-410-2	Sequence 2, Appli
4	463	100.0	86	13	US-10-054-873-4	Sequence 4, Appli
5	463	100.0	86	14	US-10-444-326-2	Sequence 2, Appli
6	463	100.0	86	15	US-10-271-869-4	Sequence 4, Appli
7	463	100.0	86	15	US-10-444-262-2	Sequence 2, Appli
8	463	100.0	86	15	US-10-444-649-2	Sequence 2, Appli
9	463	100.0	86	15	US-10-444-701-2	Sequence 2, Appli
10	463	100.0	86	17	US-10-760-928-2	Sequence 2, Appli
11	463	100.0	96	9	US-09-947-563-4	Sequence 4, Appli
12	463	100.0	110	9	US-09-205-658-125	Sequence 125, App
13	463	100.0	110	9	US-09-815-229-3	Sequence 3, Appli
14	463	100.0	110	9	US-09-804-409A-9	Sequence 9, Appli
15	463	100.0	110	10	US-09-969-748C-6	Sequence 6, Appli
16	463	100.0	110	10	US-09-963-693-125	Sequence 125, App
17	463	100.0	110	14	US-10-038-686-1	Sequence 1, Appli
18	463	100.0	110	14	US-10-328-813-2	Sequence 2, Appli
19	463	100.0	110	15	US-10-383-285-2	Sequence 2, Appli
20	463	100.0	110	15	US-10-346-563-2	Sequence 2, Appli
21	463	100.0	110	15	US-10-321-717-2	Sequence 2, Appli
22	463	100.0	110	15	US-10-411-037-44	Sequence 44, Appl
23	463	100.0	110	15	US-10-411-026-44	Sequence 44, Appl
24	463	100.0	110	15	US-10-410-962-44	Sequence 44, Appl
25	463	100.0	110	15	US-10-411-049-44	Sequence 44, Appl
26	463	100.0	110	15	US-10-700-725-20	Sequence 20, Appl
27	463	100.0	110	16	US-10-410-930-44	Sequence 44, Appl
28	463	100.0	110	16	US-10-410-997-44	Sequence 44, Appl
29	463	100.0	110	16	US-10-411-012-44	Sequence 44, Appl
30	463	100.0	110	16	US-10-287-994-44	Sequence 44, Appl
31	463	100.0	110	16	US-10-740-098-3	Sequence 3, Appli
32	463	100.0	110	16	US-10-410-913-44	Sequence 44, Appl
33	463	100.0	117	9	US-09-280-030-63	Sequence 63, Appl
34	463	100.0	130	9	US-09-280-030-62	Sequence 62, Appl
35	457	98.7	96	9	US-09-947-563-5	Sequence 5, Appli
36	442	95.5	110	16	US-10-419-539-5	Sequence 5, Appli
37	438.5	94.7	124	15	US-10-221-677-24	Sequence 24, Appl
38	388	83.8	86	17	US-10-760-928-1	Sequence 1, Appli
39	383	82.7	84	17	US-10-760-928-3	Sequence 3, Appli
40	366.5	79.2	81	17	US-10-760-928-4	Sequence 4, Appli
41	306	66.1	166	9	US-09-925-297-805	Sequence 805, App
42	300	64.8	56	9	US-09-815-229-10	Sequence 10, Appl
43	300	64.8	56	16	US-10-740-098-10	Sequence 10, Appl
44	285	61.6	54	9	US-09-815-229-13	Sequence 13, Appl
45	285	61.6	54	16	US-10-740-098-13	Sequence 13, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-878-380-1

; Sequence 1, Application US/09878380

; Patent No. US20020160435A1

```
; GENERAL INFORMATION:
; APPLICANT: Fujirebio Inc.
; APPLICANT: KITAJIMA, Sachiko
; APPLICANT: KURANO, Yoshihiro
; APPLICANT: NAKATSUBO, Kaoru
; APPLICANT: NISHIZONO, Isao
; TITLE OF INVENTION: Immunoassay For Measuring Human C-Peptide and Kit
Therefor
; FILE REFERENCE: 0760-0291P
; CURRENT APPLICATION NUMBER: US/09/878,380
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2000-174691
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-878-380-1
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Query Match          100.0%; Score 463; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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# RESULT 2

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US-09-858-935B-4
; Sequence 4, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-935B-4
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Query Match 100.0%; Score 463; DB 10; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.3e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|  
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 3

US-10-028-410-2

; Sequence 2, Application US/10028410  
; Publication No. US20020160955A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubaquier, Yves  
; APPLICANT: Lowman, Henry  
; TITLE OF INVENTION: PROTEIN VARIANTS  
; FILE REFERENCE: P1712R1-1  
; CURRENT APPLICATION NUMBER: US/10/028,410  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US/09/477,924  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 2  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-028-410-2

Query Match 100.0%; Score 463; DB 13; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.3e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
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Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 4

US-10-054-873-4

; Sequence 4, Application US/10054873  
; Publication No. US20020164712A1  
; GENERAL INFORMATION:  
; APPLICANT: Gan, Zhong Ru  
; TITLE OF INVENTION: Intramolecular Chaperone-Like Sequence  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP

```

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,873
; FILING DATE: 22-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CN98/00052
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: US 09/423,100
; FILING DATE: 11-DEC-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Mycroft, Frank J
; REGISTRATION NUMBER: 46,946
; REFERENCE/DOCKET NUMBER: 020167-000130US
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-054-873-4

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```

Query Match          100.0%; Score 463; DB 13; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86

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RESULT 5
US-10-444-326-2
; Sequence 2, Application US/10444326
; Publication No. US20030191065A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/10/444,326
; CURRENT FILING DATE: 2003-05-22

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Query Match          100.0%;  Score 463;  DB 14;  Length 86;
Best Local Similarity 100.0%;  Pred. No. 1.3e-44;
Matches    86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1  FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
             |||
Db          1  FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy          61  SLQKRGIVEQCCTSICSLYQLENYCN 86
             |||
Db          61  SLQKRGIVEQCCTSICSLYQLENYCN 86

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US-10-271-869-4

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; Sequence 4, Application US/10271869
; Publication No. US20030211992A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquin, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/10/271,869
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/09/858,935
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-271-869-4

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Query Match          100.0%;  Score 463;  DB 15;  Length 86;
Best Local Similarity 100.0%;  Pred. No. 1.3e-44;
Matches 86;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

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Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|||||  
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 7  
US-10-444-262-2  
; Sequence 2, Application US/10444262  
; Publication No. US20040023883A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubaquie, Yves  
; APPLICANT: Lowman, Henry  
; TITLE OF INVENTION: PROTEIN VARIANTS  
; FILE REFERENCE: P1712R1  
; CURRENT APPLICATION NUMBER: US/10/444,262  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/724,478  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/477,923  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 2  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-444-262-2

Query Match 100.0%; Score 463; DB 15; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.3e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|||||  
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|||||  
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 8  
US-10-444-649-2  
; Sequence 2, Application US/10444649  
; Publication No. US20040033951A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubaquie, Yves  
; APPLICANT: Lowman, Henry  
; TITLE OF INVENTION: PROTEIN VARIANTS  
; FILE REFERENCE: P1712R1  
; CURRENT APPLICATION NUMBER: US/10/444,649  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/724,479  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/477,923  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 2

; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-444-649-2

Query Match 100.0%; Score 463; DB 15; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.3e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|  
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

#### RESULT 9

US-10-444-701-2  
; Sequence 2, Application US/10444701  
; Publication No. US20040033952A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubaquie, Yves  
; APPLICANT: Lowman, Henry  
; TITLE OF INVENTION: PROTEIN VARIANTS  
; FILE REFERENCE: P1712R1  
; CURRENT APPLICATION NUMBER: US/10/444,701  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/723,866  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/477,923  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 2  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-444-701-2

Query Match 100.0%; Score 463; DB 15; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.3e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
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Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

#### RESULT 10

US-10-760-928-2  
; Sequence 2, Application US/10760928  
; Publication No. US20050026826A1

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; GENERAL INFORMATION:
; APPLICANT: HOENIG, MARGARETHE
; TITLE OF INVENTION: FELINE PROINSULIN, INSULIN AND CONSTITUENT PEPTIDES
; FILE REFERENCE: 235.00520101
; CURRENT APPLICATION NUMBER: US/10/760,928
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/440,964
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/444,009
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-760-928-2
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Query Match          100.0%;  Score 463;  DB 17;  Length 86;
Best Local Similarity 100.0%;  Pred. No. 1.3e-44;
Matches 86;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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QY      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

QY      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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# RESULT 11

US-09-947-563-4

; Sequence 4, Application US/09947563

; Patent No. US20020156234A1

; GENERAL INFORMATION:

; APPLICANT: Rubroder, Franz-Josef

; Keller, Reinhold

; TITLE OF INVENTION: Improved process for obtaining

; insulin precursors having correctly bonded cystine  
bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &

; Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/947,563

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;      FILING DATE: 07-Sep-2001
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 09/134,836
;      FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Leslie McDonell
;      REGISTRATION NUMBER: 34,872
;      REFERENCE/DOCKET NUMBER: 02481.1600-00000
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (202) 408-4000
;      TELEFAX: (202) 408-4400
;      INFORMATION FOR SEQ ID NO: 4:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 96 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      ORIGINAL SOURCE:
;      ORGANISM: Escherichia coli
;      FEATURE:
;      NAME/KEY: Protein
;      LOCATION: 1..96
;      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-563-4

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Query Match          100.0%;  Score 463;  DB 9;  Length 96;
Best Local Similarity 100.0%;  Pred. No. 1.5e-44;
Matches    86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 70

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||||||
Db      71 SLQKRGIVEQCCTSICSLYQLENYCN 96

```

# RESULT 12

US-09-205-658-125

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; Sequence 125, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080

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; EARLIER FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 125  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-205-658-125

Query Match 100.0%; Score 463; DB 9; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.8e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
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Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 13

US-09-815-229-3

; Sequence 3, Application US/09815229.  
; Patent No. US20020058614A1  
; GENERAL INFORMATION:  
; APPLICANT: Filvaroff, Ellen H.  
; APPLICANT: Okumu, Franklin W.  
; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS  
DISORDERS  
; FILE REFERENCE: P1786R1US  
; CURRENT APPLICATION NUMBER: US/09/815,229  
; CURRENT FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 60/192,103  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 3  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-815-229-3

Query Match 100.0%; Score 463; DB 9; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.8e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|  
Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 14

: PRIOR APPLICATION NUMBER: US 60/237,929

; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-969-748C-6

Query Match 100.0%; Score 463; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.8e-44;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
|  
Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84  
  
Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
|  
Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

Search completed: February 11, 2005, 19:03:52  
Job time : 63.5166 secs



OM protein - protein search, using sw model

Run on: February 11, 2005, 17:42:04 ; Search time 75.0517 Seconds  
 (without alignments)  
 586.780 Million cell updates/sec

Title: US-10-054-873-4  
 Perfect score: 463  
 Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	463	100.0	110	1	INS_GORGO	Q6yk33	gorilla gor
2	463	100.0	110	1	INS_HUMAN	P01308	homo sapien
3	463	100.0	110	1	INS_PANTR	P30410	pan troglod
4	463	100.0	110	1	INS_PONPY	Q8hxxv2	pongo pygma
5	456	98.5	110	1	INS_CERAE	P30407	cercopithec
6	456	98.5	110	1	INS_MACFA	P30406	macaca fasc
7	424	91.6	110	1	INS_RABIT	P01311	oryctolagus
8	417	90.1	110	1	INS_CANFA	P01321	canis famil
9	413	89.2	110	1	INS_SPETR	Q91xi3	spermophilu
10	394	85.1	86	1	INS_HORSE	P01310	equus cabal
11	394	85.1	110	1	INS2_MOUSE	P01326	mus musculu
12	394	85.1	110	1	INS2_RAT	P01323	rattus norv
13	392	84.7	108	1	INS_AOTTR	P67972	aotus trivi
14	392	84.7	110	1	INS_CRIL0	P01313	cricetulus
15	388	83.8	110	2	Q8WNW6	Q8wnw6	felis silve

16	385	83.2	110	1	INS1_RAT	P01322	rattus norv
17	383	82.7	108	1	INS_PIG	P01315	sus scrofa
18	377	81.4	110	1	INS_PSAOB	Q62587	psammomys o
19	366.5	79.2	105	1	INS_BOVIN	P01317	bos taurus
20	366	79.0	108	1	INS1_MOUSE	P01325	mus musculu
21	362.5	78.3	105	1	INS_SHEEP	P01318	ovis aries
22	342	73.9	65	2	Q8HZ80	Q8hz80	pongo pygma
23	342	73.9	65	2	Q8HZ81	Q8hz81	gorilla gor
24	334.5	72.2	108	1	INS_RODSP	P21563	rodentia sp
25	314	67.8	110	1	INS_CAVPO	P01329	cavia porce
26	277.5	59.9	109	1	INS_OCTDE	P17715	octodon deg
27	276.5	59.7	103	1	INS_SELRF	P51463	selasphorus
28	265.5	57.3	106	1	INS2_XENLA	P12707	xenopus lae
29	265.5	57.3	107	1	INS_CHICK	P67970	gallus gall
30	262.5	56.7	106	1	INS1_XENLA	P12706	xenopus lae
31	256.5	55.4	51	1	INS_BALPH	P67973	balaenopter
32	256.5	55.4	51	1	INS_ELEMA	P01316	elephas max
33	256.5	55.4	51	1	INS_PHYCA	P67974	physeter ca
34	256.5	55.4	81	1	INS_ANAPL	P01333	anas platyr
35	256	55.3	96	2	Q7MOU6	Q7m0u6	bacillus br
36	254.5	55.0	51	2	Q7MOG1	Q7m0g1	cricetidae
37	251.5	54.3	51	1	INS_ACOCA	P01324	acomys cahi
38	250.5	54.1	51	2	Q7M217	Q7m217	canavalia e
39	246.5	53.2	51	1	INS_BALBO	P01314	balaenopter
40	246.5	53.2	51	1	INS_CAMDR	P01320	camelus dro
41	246.5	53.2	51	1	INS_CAPHI	P01319	capra hircu
42	246.5	53.2	106	2	Q9I8Q7	Q9i8q7	rana pipien
43	245.5	53.0	51	1	INS_FELCA	P06306	felis silve
44	244.5	52.8	51	1	INS_SAISC	P67971	saimiri sci
45	239.5	51.7	51	1	INS_DIDMA	P18109	didelphis m

#### ALIGNMENTS

##### RESULT 1

##### INS\_GORGO

ID INS\_GORGO STANDARD; PRT; 110 AA.

AC Q6YK33;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Insulin precursor.

GN Name=INS;

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI\_TaxID=9595;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;

RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;

RT "Global haplotype diversity in the human insulin gene region.";

RL Genome Res. 13:2101-2111(2003).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It

CC increases cell permeability to monosaccharides, amino acids and

CC fatty acids. It accelerates glycolysis, the pentose phosphate

CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AY137500; AAN06935.1; -.  
 DR InterPro; IPR004825; Ins/IGF/relax.  
 DR InterPro; IPR003234; Mollusc\_ins.  
 DR Pfam; PF00049; Insulin; 1.  
 DR PRINTS; PR00277; INSULINB.  
 DR ProDom; PD015667; Mollusc\_ins; 1.  
 DR SMART; SM00078; ILGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Glucose metabolism; Hormone; Insulin family; Signal.  
 FT SIGNAL 1 24 By similarity.  
 FT CHAIN 25 54 Insulin B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin A chain.  
 FT DISULFID 31 96 Interchain (By similarity).  
 FT DISULFID 43 109 Interchain (By similarity).  
 FT DISULFID 95 100 By similarity.  
 SQ SEQUENCE 110 AA; 11981 MW; C2C3B23B85E520E5 CRC64;

Query Match 100.0%; Score 463; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 8e-41;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84  
 QY 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||  
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

## RESULT 2

### INS\_HUMAN

ID INS\_HUMAN STANDARD; PRT; 110 AA.  
 AC P01308;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Insulin precursor.  
 GN Name=INS;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80120725; PubMed=6243748;  
 RA Bell G.I., Pictet R.L., Rutter W.J., Cordell B., Tischer E.,  
 RA Goodman H.M.;  
 RT "Sequence of the human insulin gene.";  
 RL Nature 284:26-32(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80236313; PubMed=6248962;  
 RA Ullrich A., Dull T.J., Gray A., Brosius J., Sures I.;  
 RT "Genetic variation in the human insulin gene.";  
 RL Science 209:612-615(1980).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80054779; PubMed=503234;  
 RA Bell G.I., Swain W.F., Pictet R.L., Cordell B., Goodman H.M.,  
 RA Rutter W.J.;  
 RT "Nucleotide sequence of a cDNA clone encoding human preproinsulin.";  
 RL Nature 282:525-527(1979).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80147417; PubMed=6927840;  
 RA Sures I., Goeddel D.V., Gray A., Ullrich A.;  
 RT "Nucleotide sequence of human preproinsulin complementary DNA.";  
 RL Science 208:57-59(1980).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93364428; PubMed=8358440;  
 RA Lucassen A.M., Bell J.I., Julier C., Lathrop M.;  
 RT "Susceptibility to insulin dependent diabetes mellitus maps to a 4.1  
 RT kb segment of DNA spanning the insulin gene and associated VNTR.";  
 RL Nat. Genet. 4:305-310(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";

RI. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP SEQUENCE OF 1-59 FROM N.A.  
 RC TISSUE=Blood;  
 RA Fajardy I.I., Weill J.J., Stuckens C.C., Danze P.M.P.;  
 RT "Description of a novel RFLP diallelic polymorphism (-127 BsgI C/G)  
 RT within the 5' region of insulin gene.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [8]  
 RP SEQUENCE OF 25-54 AND 90-110.  
 RX PubMed=14426955;  
 RA Nicol D.S.H.W., Smith L.F.;  
 RT "Amino-acid sequence of human insulin.";  
 RL Nature 187:483-485(1960).  
 RN [9]  
 RP SEQUENCE OF 57-87.  
 RX MEDLINE=71116410; PubMed=5101771;  
 RA Oyer P.E., Cho S., Peterson J.D., Steiner D.F.;  
 RT "Studies on human proinsulin. Isolation and amino acid sequence of the  
 RT human pancreatic C-peptide.";  
 RL J. Biol. Chem. 246:1375-1386(1971).  
 RN [10]  
 RP SEQUENCE OF 57-87.  
 RX MEDLINE=71257722; PubMed=5560404;  
 RA Ko A., Smyth D.G., Markussen J., Sundby F.;  
 RT "The amino acid sequence of the C-peptide of human proinsulin.";  
 RL Eur. J. Biochem. 20:190-199(1971).  
 RN [11]  
 RP SYNTHESIS.  
 RX MEDLINE=75077277; PubMed=4443293;  
 RA Sieber P., Kamber B., Hartmann A., Joehl A., Riniker B., Rittel W.;  
 RT "Total synthesis of human insulin under directed formation of the  
 RT disulfide bonds.";  
 RL Helv. Chim. Acta 57:2617-2621(1974).  
 RN [12]  
 RP SYNTHESIS OF 57-87.  
 RX MEDLINE=75040007; PubMed=4803504;  
 RA Naithani V.K.;  
 RT "Studies on polypeptides, IV. The synthesis of C-peptide of human  
 RT proinsulin.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:659-672(1973).  
 RN [13]  
 RP SYNTHESIS OF 65-69 AND 70-73.  
 RX MEDLINE=73161263; PubMed=4698555;  
 RA Geiger R., Volk A.;  
 RT "Synthesis of peptides with the properties of human proinsulin C  
 RT peptides (hC peptide). 3. Synthesis of the sequences 14-17 and 9-13 of  
 RT human proinsulin C peptides.";  
 RL Chem. Ber. 106:199-205(1973).  
 RN [14]  
 RP SYNTHESIS OF 84-87.  
 RX MEDLINE=73161261; PubMed=4698553;  
 RA Geiger R., Jaeger G., Keonig W., Treuth G.;  
 RT "Synthesis of peptides with the properties of human proinsulin C  
 RT peptides (hC peptide). I. Scheme for the synthesis and preparation of  
 RT the sequence 28-31 of human proinsulin C peptide.";  
 RL Chem. Ber. 106:188-192(1973).

RN [15]  
 RP VARIANT LOS ANGELES SER-48.  
 RX MEDLINE=84016053; PubMed=6312455;  
 RA Haneda M., Chan S.J., Kwok S.C.M., Rubenstein A.H., Steiner D.F.;  
 RT "Studies on mutant human insulin genes: identification and sequence  
 RT analysis of a gene encoding [SerB24]insulin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6366-6370(1983).  
 RN [16]  
 RP VARIANTS LOS ANGELES SER-48 AND CHICAGO LEU-49.  
 RX MEDLINE=84170233; PubMed=6424111;  
 RA Shoelson S., Fickova M., Haneda M., Nahum A., Musso G., Kaiser E.T.,  
 RA Rubenstein A.H., Tager H.;  
 RT "Identification of a mutant human insulin predicted to contain a  
 RT serine-for-phenylalanine substitution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7390-7394(1983).  
 RN [17]  
 RP VARIANT PROVIDENCE ASP-34.  
 RX MEDLINE=87175640; PubMed=3470784;  
 RA Chan S.J., Seino S., Gruppuso P.A., Schwartz R., Steiner D.F.;  
 RT "A mutation in the B chain coding region is associated with impaired  
 RT proinsulin conversion in a family with hyperproinsulinemia.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2194-2197(1987).  
 RN [18]  
 RP VARIANT WAKAYAMA LEU-92.  
 RX MEDLINE=87058122; PubMed=3537011;  
 RA Sakura H., Iwamoto Y., Sakamoto Y., Kuzuya T., Hirata H.;  
 RT "Structurally abnormal insulin in a diabetic patient. Characterization  
 RT of the mutant insulin A3 (Val-->Leu) isolated from the pancreas.";  
 RL J. Clin. Invest. 78:1666-1672(1986).  
 RN [19]  
 RP VARIANT HIS-89.  
 RX MEDLINE=90317021; PubMed=2196279;  
 RA Barbetti F., Raben N., Kadowaki T., Cama A., Accili D., Gabbay K.H.,  
 RA Merenich J.A., Taylor S.I., Roth J.;  
 RT "Two unrelated patients with familial hyperproinsulinemia due to a  
 RT mutation substituting histidine for arginine at position 65 in the  
 RT proinsulin molecule: identification of the mutation by direct  
 RT sequencing of genomic deoxyribonucleic acid amplified by polymerase  
 RT chain reaction.";  
 RL J. Clin. Endocrinol. Metab. 71:164-169(1990).  
 RN [20]  
 RP VARIANT HIS-89.  
 RX MEDLINE=85261996; PubMed=4019786;  
 RA Shibasaki Y., Kawakami T., Kanazawa Y., Akanuma Y., Takaku F.;  
 RT "Posttranslational cleavage of proinsulin is blocked by a point  
 RT mutation in familial hyperproinsulinemia.";  
 RL J. Clin. Invest. 76:378-380(1985).  
 RN [21]  
 RP VARIANT KYOTO LEU-89.  
 RX MEDLINE=92291307; PubMed=1601997;  
 RA Yano H., Kitano N., Morimoto M., Polonsky K.S., Imura H., Seino Y.;  
 RT "A novel point mutation in the human insulin gene giving rise to  
 RT hyperproinsulinemia (proinsulin Kyoto).";  
 RL J. Clin. Invest. 89:1902-1907(1992).  
 RN [22]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=91104966; PubMed=2271664;

RA Hua Q.-X., Weiss M.A.;  
 RT "Toward the solution structure of human insulin: sequential 2D 1H NMR  
 RT assignment of a des-pentapeptide analogue and comparison with crystal  
 RT structure.";  
 RL Biochemistry 29:10545-10555(1990).  
 RN [23]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=91242467; PubMed=2036420;  
 RA Hua Q.-X., Weiss M.A.;  
 RT "Comparative 2D NMR studies of human insulin and des-pentapeptide  
 RT insulin: sequential resonance assignment and implications for protein  
 RT dynamics and receptor recognition.";  
 RL Biochemistry 30:5505-5515(1991).  
 RN [24]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=91265527; PubMed=1646635; DOI=10.1016/0167-4838(91)90098-K;  
 RA Hua Q.-X., Weiss M.A.;  
 RT "Two-dimensional NMR studies of Des-(B26-B30)-insulin: sequence-  
 RT specific resonance assignments and effects of solvent composition.";

Query Match 100.0%; Score 463; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 8e-41;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||||||||||  
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 3  
 INS\_PANTR

ID INS\_PANTR STANDARD; PRT; 110 AA.  
 AC P30410;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Insulin precursor.  
 GN Name=INS;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92219953; PubMed=1560757;  
 RA Seino S., Bell G.I., Li W.;  
 RT "Sequences of primate insulin genes support the hypothesis of a slower  
 RT rate of molecular evolution in humans and apes than in monkeys.";  
 RL Mol. Biol. Evol. 9:193-203(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;  
 RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;

RT "Global haplotype diversity in the human insulin gene region.";  
 RL Genome Res. 13:2101-2111(2003).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X61089; CAA43403.1; -.  
 DR EMBL; AY137497; AAN06933.1; -.  
 DR PIR; A42179; A42179.  
 DR HSSP; P01308; 1AI0.  
 DR InterPro; IPR004825; Ins/IGF/relax.  
 DR Pfam; PF00049; Insulin; 1.  
 DR PRINTS; PR00277; INSULINB.  
 DR ProDom; PD015667; Mollusc\_ins; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Glucose metabolism; Hormone; Insulin family; Signal.  
 FT SIGNAL 1 24 By similarity.  
 FT CHAIN 25 54 Insulin B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin A chain.  
 FT DISULFID 31 96 Interchain (By similarity).  
 FT DISULFID 43 109 Interchain (By similarity).  
 FT DISULFID 95 100 By similarity.  
 SQ SEQUENCE 110 AA; 12025 MW; 41EB8DF79837CEF5 CRC64;

Query Match 100.0%; Score 463; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 8e-41;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||  
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

#### RESULT 4

INS\_PONPY

ID INS\_PONPY STANDARD; PRT; 110 AA.

AC Q8HXV2;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)



DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Insulin precursor.  
 GN Name=INS;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;  
 RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;  
 RT "Global haplotype diversity in the human insulin gene region.";  
 RL Genome Res. 13:2101-2111(2003).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----  
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 CC -----  
 DR EMBL; AY137503; AAN06937.1; -.  
 DR HSSP; P01308; 1AI0.  
 DR InterPro; IPR004825; Ins/IGF/relax.  
 DR Pfam; PF00049; Insulin; 1.  
 DR PRINTS; PR00277; INSULINB.  
 DR ProDom; PD015667; Mollusc\_ins; 1.  
 DR SMART; SM00078; ILGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Glucose metabolism; Hormone; Insulin family; Signal.  
 FT SIGNAL 1 24 By similarity.  
 FT CHAIN 25 54 Insulin B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin A chain.  
 FT DISULFID 31 96 Interchain (By similarity).  
 FT DISULFID 43 109 Interchain (By similarity).  
 FT DISULFID 95 100 By similarity.  
 SQ SEQUENCE 110 AA; 12038 MW; 22D2B32B94F520F8 CRC64;  
  
 Query Match 100.0%; Score 463; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 8e-41;  
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84  
  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

|||||  
Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 5

INS\_CERAE

ID INS\_CERAE STANDARD; PRT; 110 AA.  
AC P30407; P01309;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Insulin precursor.  
GN Name=INS;  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92219953; PubMed=1560757;  
RA Seino S., Bell G.I., Li W.;  
RT "Sequences of primate insulin genes support the hypothesis of a slower  
RT rate of molecular evolution in humans and apes than in monkeys."  
RL Mol. Biol. Evol. 9:193-203(1992).  
RN [2]  
RP SEQUENCE OF 57-87.  
RX MEDLINE=72258016; PubMed=4626369;  
RA Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.;  
RT "Determination of the amino acid sequence of the monkey, sheep, and  
RT dog proinsulin C-peptides by a semi-micro Edman degradation  
RT procedure."  
RL J. Biol. Chem. 247:4866-4871(1972).  
CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
CC increases cell permeability to monosaccharides, amino acids and  
CC fatty acids. It accelerates glycolysis, the pentose phosphate  
CC cycle, and glycogen synthesis in liver.  
CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
CC disulfide bonds.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the insulin family.  
CC -----  
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CC -----  
DR EMBL; X61092; CAA43405.1; -.  
DR PIR; B42179; B42179.  
DR HSSP; P01308; 1AI0.  
DR InterPro; IPR004825; Ins/IGF/relax.  
DR Pfam; PF00049; Insulin; 1.  
DR PRINTS; PR00277; INSULINB.  
DR ProDom; PD015667; Mollusc\_ins; 1.

DR SMART; SM00078; IIGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Direct protein sequencing; Glucose metabolism; Hormone;  
 KW Insulin family; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 54 Insulin B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin A chain.  
 FT DISULFID 31 96 Interchain.  
 FT DISULFID 43 109 Interchain.  
 FT DISULFID 95 100  
 SQ SEQUENCE 110 AA; 12019 MW; 95A1F54BE7B247F9 CRC64;

Query Match 98.5%; Score 456; DB 1; Length 110;  
 Best Local Similarity 98.8%; Pred. No. 4.3e-40;  
 Matches 85; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLALEG 84  
 Qy 61 SLQKRGIIVEQCCTSICSLYQLENYCN 86  
 ||||||||||||||||||||  
 Db 85 SLQKRGIIVEQCCTSICSLYQLENYCN 110

# RESULT 6

## INS\_MACFA

ID INS\_MACFA STANDARD; PRT; 110 AA.  
 AC P30406; P01309;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Insulin precursor.  
 GN Name=INS;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83080474; PubMed=6184262; DOI=10.1016/0378-1119(82)90004-X;  
 RA Wetekam W., Groneberg J., Leineweber M., Wengenmayer F.,  
 RA Winnacker E.-L.;  
 RT "The nucleotide sequence of cDNA coding for preproinsulin from the  
 RT primate Macaca fascicularis."  
 RL Gene 19:179-183(1982).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----



RA Devaskar S.U., Giddings S.J., Rajakumar P.A., Carnaghi L.R.,  
 RA Menon R.K., Zahm D.S.;  
 RT "Insulin gene expression and insulin synthesis in mammalian neuronal  
 RT cells.";  
 RL J. Biol. Chem. 269:8445-8454(1994).  
 RN [2]  
 RP SEQUENCE OF 25-54 AND 90-110.  
 RX MEDLINE=66160119; PubMed=5949593; DOI=10.1016/0002-9343(66)90145-8;  
 RA Smith L.F.;  
 RT "Species variation in the amino acid sequence of insulin.";  
 RL Am. J. Med. 40:662-666(1966).  
 RN [3]  
 RP SEQUENCE OF 56-110 FROM N.A.  
 RA Giddings S.J., Carnaghi L.R., Devaskar S.U.;  
 RL Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----  
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 CC -----  
 DR EMBL; U03610; AAA19033.1; -.  
 DR EMBL; M61153; AAA17540.1; -.  
 DR PIR; A53438; INRB.  
 DR HSSP; P01308; 1EV6.  
 DR InterPro; IPR004825; Ins/IGF/relax.  
 DR Pfam; PF00049; Insulin; 1.  
 DR PRINTS; PR00277; INSULINB.  
 DR ProDom; PD015667; Mollusc\_ins; 1.  
 DR SMART; SM00078; IIGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Direct protein sequencing; Glucose metabolism; Hormone;  
 KW Insulin family; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 54 Insulin B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin A chain.  
 FT DISULFID 31 96 Interchain.  
 FT DISULFID 43 109 Interchain.  
 FT DISULFID 95 100  
 FT CONFLICT 83 83 E -> Y (in Ref. 3).  
 SQ SEQUENCE 110 AA; 11838 MW; 82D2975B85D77FA8 CRC64;  
  
 Query Match 91.6%; Score 424; DB 1; Length 110;  
 Best Local Similarity 90.7%; Pred. No. 1e-36;  
 Matches 78; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 |||||:||||| ||||| ||| |||  
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKSRREVEELQVGQAEELGGGPGAGGLQPSALEL 84

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 :|||||  
 Db 85 ALQKRGIVEQCCTSICSLYQLENYCN 110

# RESULT 8

## INS\_CANFA

ID INS\_CANFA STANDARD; PRT; 110 AA.  
 AC P01321;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Insulin precursor.  
 GN Name=INS;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83109071; PubMed=6296142;  
 RA Kwok S.C.M., Chan S.J., Steiner D.F.;  
 RT "Cloning and nucleotide sequence analysis of the dog insulin gene.  
 RT Coded amino acid sequence of canine preproinsulin predicts an  
 RT additional C-peptide fragment.";  
 RL J. Biol. Chem. 258:2357-2363(1983).  
 RN [2]  
 RP SEQUENCE OF 25-54 AND 90-110.  
 RX MEDLINE=66160119; PubMed=5949593; DOI=10.1016/0002-9343(66)90145-8;  
 RA Smith L.F.;  
 RT "Species variation in the amino acid sequence of insulin.";  
 RL Am. J. Med. 40:662-666(1966).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----  
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 CC -----  
 DR EMBL; V00179; CAA23475.1; -.  
 DR PIR; A92413; IPDG.  
 DR HSSP; P01317; 1APH.

DR InterPro; IPR004825; Ins/IGF/relax.  
 DR Pfam; PF00049; Insulin; 1.  
 DR PRINTS; PR00277; INSULINB.  
 DR ProDom; PD015667; Mollusc\_ins; 1.  
 DR SMART; SM00078; IIGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Direct protein sequencing; Glucose metabolism; Hormone;  
 KW Insulin family; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 54 Insulin B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin A chain.  
 FT DISULFID 31 96 Interchain.  
 FT DISULFID 43 109 Interchain.  
 FT DISULFID 95 100  
 SQ SEQUENCE 110 AA; 12190 MW; A574791864A4FB98 CRC64;

Query Match 90.1%; Score 417; DB 1; Length 110;  
 Best Local Similarity 89.5%; Pred. No. 5.4e-36;  
 Matches 77; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 |||||  
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEDLQVRDELAPGEGGLQPLALEG 84  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 :|||  
 Db 85 ALQKRGIVEQCCTSICSLYQLENYCN 110

# RESULT 9

## INS\_SPETR

ID INS\_SPETR STANDARD; PRT; 110 AA.  
 AC Q91XI3;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Insulin precursor.  
 GN Name=INS;  
 OS *Spermophilus tridecemlineatus* (Thirteen-lined ground squirrel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC *Spermophilus*.  
 OX NCBI\_TaxID=43179;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Tredrea M.M., Buck M.J., Guhaniyogi J., Squire T.L., Andrews M.T.;  
 RT "Regulation of PDK4 expression in a hibernating mammal."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the insulin family.

```

DR      EMBL; AY038604; AAK72558.1; -.
DR      HSSP; P01308; 1EV6.
DR      InterPro; IPR004825; Ins/IGF/relax.
DR      Pfam; PF00049; Insulin; 1.
DR      PRINTS; PR00277; INSULINB.
DR      ProDom; PD015667; Mollusc_ins; 1.
DR      SMART; SM00078; IIGF; 1.
DR      PROSITE; PS00262; INSULIN; 1.
KW      Glucose metabolism; Hormone; Insulin family; Signal.
FT      SIGNAL          1      24      By similarity.
FT      CHAIN           25      54      Insulin B chain.
FT      PROPEP          57      87      C peptide.
FT      CHAIN           90     110      Insulin A chain.
FT      DISULFID        31      96      Interchain (By similarity).
FT      DISULFID        43     109      Interchain (By similarity).
FT      DISULFID        95     100      By similarity.
SQ      SEQUENCE      110 AA;  12004 MW;  4511768D6622BEE5 CRC64;

```

```

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        |||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKSRREVEEQQGGQVELGGGPGAGLPQPLALEM 84
        |||
Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        :|||
Db      85 ALQKRGIVEQCCTSICSLYQLENYCN 110

```





DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Insulin 2 precursor.  
 GN Name=Ins2; Synonyms=Ins-2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87169768; PubMed=3104603;  
 RA Wentworth B.M., Schaefer I.M., Villa-Komaroff L., Chirgwin J.M.;  
 RT "Characterization of the two nonallelic genes encoding mouse  
 RT preproinsulin.";  
 RL J. Mol. Evol. 23:305-312(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NON;  
 RX MEDLINE=90372989; PubMed=2397023;  
 RA Sawa T., Ohgaku S., Morioka H., Yano S.;  
 RT "Molecular cloning and DNA sequence analysis of preproinsulin genes in  
 RT the NON mouse, an animal model of human non-obese, non-insulin-  
 RT dependent diabetes mellitus.";  
 RL J. Mol. Endocrinol. 5:61-67(1990).  
 RN [3]  
 RP SEQUENCE OF 25-54 AND 90-110.  
 RX MEDLINE=72189455; PubMed=5063718;  
 RA Buenzli H.F., Glatthaar B., Kunz P., Muelhaupt E., Humbel R.E.;  
 RT "Amino acid sequence of the two insulins from mouse (Maus musculus).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:451-458(1972).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----  
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 CC -----  
 DR EMBL; X04724; CAA28433.1; -.  
 DR PIR; A26342; INMS2.  
 DR HSSP; P01317; 1APH.  
 DR MGD; MGI:96573; Ins2.  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IDA.  
 DR GO; GO:0000187; P:activation of MAPK; IDA.  
 DR GO; GO:0006006; P:glucose metabolism; IMP.  
 DR GO; GO:0008286; P:insulin receptor signaling pathway; IDA.  
 DR GO; GO:0016042; P:lipid catabolism; IDA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IMP.

DR GO; GO:0042325; P:regulation of phosphorylation; IDA.  
 DR GO; GO:0006983; P:response to ER-overload; IMP.  
 DR InterPro; IPR004825; Ins/IGF/relax.  
 DR Pfam; PF00049; Insulin; 1.  
 DR PRINTS; PR00277; INSULINB.  
 DR ProDom; PD015667; Mollusc\_ins; 1.  
 DR SMART; SM00078; IIGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Direct protein sequencing; Glucose metabolism; Hormone;  
 KW Insulin family; Multigene family; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 54 Insulin 2 B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin 2 A chain.  
 FT DISULFID 31 96 Interchain.  
 FT DISULFID 43 109 Interchain.  
 FT DISULFID 95 100  
 SQ SEQUENCE 110 AA; 12364 MW; 3554C8803D24FDAD CRC64;

Query Match 85.1%; Score 394; DB 1; Length 110;  
 Best Local Similarity 84.9%; Pred. No. 1.4e-33;  
 Matches 73; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 || ||||| :|| || || :||| || || || ||  
 Db 25 FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVEDPQVAQLLEGGGPGAGDLQTLALEV 84  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 : |||||:|||||  
 Db 85 AQQKRGIVDQCCTSICSLYQLENYCN 110

# RESULT 12

## INS2\_RAT

ID INS2\_RAT STANDARD; PRT; 110 AA.  
 AC P01323;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Insulin 2 precursor.  
 GN Name=Ins2; Synonyms=Ins-2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=80045035; PubMed=498284; DOI=10.1016/0092-8674(79)90071-0;  
 RA Lomedico P., Rosenthal N., Efstratiadis A., Gilbert W., Kolodner R.,  
 RA Tizard R.;  
 RT "The structure and evolution of the two nonallelic rat preproinsulin  
 RT genes.";  
 RL Cell 18:545-558(1979).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86310882; PubMed=2427930;

RA Soares M.B., Schin E., Henderson A., Karathanasis S.K., Cate R.,  
 RA Zeitlin S., Chirgwin J., Efstratiadis A.;  
 RT "RNA-mediated gene duplication: the rat preproinsulin I gene is a  
 RT functional retroposon.";  
 RL Mol. Cell. Biol. 5:2090-2103(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80240379; PubMed=6249167;  
 RA Lomedico P.T., Rosenthal N., Kolodner R., Efstratiadis A., Gilbert W.;  
 RT "The structure of rat preproinsulin genes.";  
 RL Ann. N. Y. Acad. Sci. 343:425-432(1980).  
 RN [4]  
 RP SEQUENCE OF 25-54 AND 90-110.  
 RX MEDLINE=70067613; PubMed=4311938;  
 RA Steiner D.F., Clark J.L., Nolan C., Rubenstein A.H., Margoliash E.,  
 RA Aten B., Oyer P.E.;  
 RT "Proinsulin and the biosynthesis of insulin.";  
 RL Recent Prog. Horm. Res. 25:207-282(1969).  
 RN [5]  
 RP SEQUENCE OF 57-87.  
 RX MEDLINE=73061498; PubMed=4640931;  
 RA Tager H.S., Steiner D.F.;  
 RT "Primary structures of the proinsulin connecting peptides of the rat  
 RT and the horse.";  
 RL J. Biol. Chem. 247:7936-7940(1972).  
 RN [6]  
 RP SEQUENCE OF 57-87, AND REVISIONS.  
 RX MEDLINE=72177385; PubMed=4554104;  
 RA Markussen J., Sundby F.;  
 RT "Rat-proinsulin C-peptides. Amino-acid sequences.";  
 RL Eur. J. Biochem. 25:153-162(1972).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
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 CC -----  
 DR EMBL; V01243; CAA24560.1; -.  
 DR EMBL; J00748; AAA41443.1; -.  
 DR EMBL; M25585; AAA41440.1; -.  
 DR EMBL; M25583; AAA41440.1; JOINED.  
 DR PIR; B90789; IPRT2.  
 DR HSSP; P01317; 1APH.  
 DR RGD; 2916; Ins2.  
 DR InterPro; IPR004825; Ins/IGF/relax.  
 DR Pfam; PF00049; Insulin; 1.

DR PRINTS; PR00277; INSULINB.  
 DR ProDom; PD015667; Mollusc\_ins; 1.  
 DR SMART; SM00078; IIGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Direct protein sequencing; Glucose metabolism; Hormone;  
 KW Insulin family; Multigene family; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 54 Insulin 2 B chain.  
 FT PROPEP 57 87 C peptide.  
 FT CHAIN 90 110 Insulin 2 A chain.  
 FT DISULFID 31 96 Interchain.  
 FT DISULFID 43 109 Interchain.  
 FT DISULFID 95 100  
 SQ SEQUENCE 110 AA; 12339 MW; 3A626DA98C86F3CA CRC64;

Query Match 85.1%; Score 394; DB 1; Length 110;  
 Best Local Similarity 84.9%; Pred. No. 1.4e-33;  
 Matches 73; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60  
 || ||||| :||| || || :||| || || |||||  
 Db 25 FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVEDPQVAQLELGGGPGAGDLQTLALEV 84  
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86  
 : |||||:|||||  
 Db 85 ARQKRGIVDQCCTSICSLYQLENYCN 110

# RESULT 13

## INS\_AOTTR

ID INS\_AOTTR STANDARD; PRT; 108 AA.  
 AC P67972; P10604;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Insulin precursor.  
 GN Name=INS;  
 OS Aotus trivirgatus (Night monkey) (Douroucouli).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 OX NCBI\_TaxID=9505;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88041119; PubMed=3118367;  
 RA Seino S., Steiner D.F., Bell G.I.;  
 RT "Sequence of a New World primate insulin having low biological potency  
 and immunoreactivity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7423-7427(1987).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 CC -----



```

RA Bell G.I., Sanchez-Pescador R.;
RT "Sequence of a cDNA encoding Syrian hamster preproinsulin.";
RL Diabetes 33:297-300(1984).
RN [2]
RP SEQUENCE OF 25-54 AND 90-110.
RA Neelon F.A., Delcher H.K., Steinman H., Lebovitz H.E.;
RT "Structure of hamster insulin: comparison with a tumor insulin.";
RL Fed. Proc. 32:300-300(1973).
CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
CC increases cell permeability to monosaccharides, amino acids and
CC fatty acids. It accelerates glycolysis, the pentose phosphate
CC cycle, and glycogen synthesis in liver.
CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
CC disulfide bonds.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the insulin family.

```

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DR      EMBL; M26328; AAA37089.1; -.
DR      HSSP; P01308; 1EV6.
DR      InterPro; IPR004825; Ins/IGF/relax.
DR      Pfam; PF00049; Insulin; 1.
DR      PRINTS; PR00277; INSULINB.
DR      ProDom; PD015667; Mollusc_ins; 1.
DR      SMART; SM00078; IIGF; 1.
DR      PROSITE; PS00262; INSULIN; 1.
KW      Direct protein sequencing; Glucose metabolism; Hormone;
KW      Insulin family; Signal.
FT      SIGNAL          1          24
FT      CHAIN           25          54      Insulin B chain.
FT      PROPEP          57          87      C peptide.
FT      CHAIN           90         110      Insulin A chain.
FT      DISULFID         31          96      Interchain.
FT      DISULFID         43         109      Interchain.
FT      DISULFID         95         100
SO      SEQUENCE        110 AA;  12268 MW;  219E92B85A535CEC CRC64;

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Query Match 84.7%; Score 392; DB 1; Length 110;  
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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQLALEG 60  
        ||| | | | | | | | | | | | | | | | : | | | | | : | | | | | | |  
Db     25 FVNQHLCGSHLVEALYLVCGERGFFYTPKSRRGVDPQVAQLELG GGPADDLT LALEV 84  
  
Qy     61 SLQKRGI VEQCCTS ICSLY QLEN YCN 86  
       : | | | | : | | | | | | | | | | | | | | | |  
Db    85 AQQKRGI VDQCCTS ICSLY QLEN YCN 110
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Q8WNW6

Query Match 83.8%; Score 388; DB 2; Length 110;  
Best Local Similarity 83.7%; Pred. No. 6.1e-33;  
Matches 72; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Search completed: February 11, 2005, 18:22:48  
Job time : 76.0517 secs